

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 27, 2003, 01:09:38 / Search time 472 Seconds
(without alignments)
4111.382 Million cell updates/sec

Title: US-09-687-230a-2
Perfect score: 3073
Sequence: 1 MGKKKKKKSKDKLHYERYE.....PGNNICLLGPSKCIILINK 589

Scoring table:
BLOSUM62
Xgapop 10.0, Ygapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 2190069 segs, 1647345023 residues
Total number of hits satisfying chosen parameters: 4380138

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=Published Applications NA -QFMT=fastap -SUFFIX=now25.tmpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=1 -MATRIX=bl0sum62
-TRANS=human40.cdt -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
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-MAXLEN=200000000 -USER=US09667230@cgn_1_1.85@runat_25112003_123734_17741
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-FCGAPOP=6 -FCGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA:*

- 1: /cg2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cg2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cg2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cg2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cg2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cg2_6/ptodata/2/pubpna/PCT_NEW_PUBCOMB.seq:*
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- 9: /cg2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cg2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 11: /cg2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cg2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
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- 16: /cg2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 17: /cg2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	3002.5	97.7	7053	10 US-09-764-864-792 Sequence 792, App

2	1263	41.1	1351	10 US-09-764-864-379 Sequence 379, App
3	921.5	30.0	2830	13 US-10-098-841-196 Sequence 196, App
4	872.5	28.4	517	10 US-09-867-701-2944 Sequence 2944, App
5	780	25.4	480	11 US-09-918-995-37236 Sequence 37236, A
6	502.5	16.4	421	10 US-09-860-352-7102 Sequence 7102, App
7	477	15.5	513	10 US-09-960-253-96 Sequence 96, App
8	359	11.7	7053	10 US-09-764-864-792 Sequence 792, App
9	274	8.9	1861	12 US-10-096-534-53 Sequence 53, App
10	258.5	8.4	4549	14 US-10-037-270-266 Sequence 266, App
11	258.5	8.4	4549	14 US-10-037-270-267 Sequence 267, App
12	227	7.4	8147	13 US-10-109-886-9 Sequence 9, App
13	219.5	7.1	1636	9 US-09-925-301-104 Sequence 104, App
14	215.5	7.0	577	9 US-09-864-761-11927 Sequence 11927, A
15	215.5	7.0	32222	14 US-09-764-887-619 Sequence 619, App
16	215.5	7.0	32222	14 US-10-073-961-619 Sequence 619, App
17	213.5	6.9	2232	9 US-09-864-761-28507 Sequence 28507, A
18	210	6.8	5959	10 US-09-954-456-1996 Sequence 1996, App
19	205	6.7	5257	12 US-10-007-926A-237 Sequence 237, App
20	205	6.7	7326	13 US-10-109-886-7 Sequence 7, App
21	201	6.5	2213	12 US-10-199-672-549 Sequence 549, App
22	201	6.5	2213	12 US-10-187-748-549 Sequence 549, App
23	201	6.5	2213	12 US-10-194-457-549 Sequence 549, App
24	201	6.5	2213	12 US-10-184-642-549 Sequence 549, App
25	201	6.5	2213	12 US-10-196-747-549 Sequence 549, App
26	201	6.5	2213	12 US-10-173-689-549 Sequence 549, App
27	201	6.5	2213	12 US-10-173-689-549 Sequence 549, App
28	201	6.5	2213	12 US-10-173-691-549 Sequence 549, App
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33	201	6.5	2213	12 US-10-173-699-549 Sequence 549, App
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35	201	6.5	2213	12 US-10-174-583-549 Sequence 549, App
36	201	6.5	2213	12 US-10-174-583-549 Sequence 549, App
37	201	6.5	2213	12 US-10-174-589-549 Sequence 549, App
38	201	6.5	2213	12 US-10-174-591-549 Sequence 549, App
39	201	6.5	2213	12 US-10-175-736-549 Sequence 549, App
40	201	6.5	2213	12 US-10-175-742-549 Sequence 549, App
41	201	6.5	2213	12 US-10-175-744-549 Sequence 549, App
42	201	6.5	2213	12 US-10-175-748-549 Sequence 549, App
43	201	6.5	2213	12 US-10-175-748-549 Sequence 549, App
44	201	6.5	2213	12 US-10-175-751-549 Sequence 549, App
45	201	6.5	2213	12 US-10-175-754-549 Sequence 549, App

ALIGNMENTS

RESULT 1
US-09-764-864-792
Sequence 792, Application US/09764864
Patent No. US20020132753A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT223
CURRENT APPLICATION NUMBER: US/09/764,864
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1792
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 792
LENGTH: 7053
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (154)
OTHER INFORMATION: n equals a,t,g, or c
US-09-764-864-792
Alignment Scores: 1.76e-295 Length: 7053
Pred. No.:

Score: 3002.50 Matches: 581
Percent Similarity: 98.98% Conservative: 1
Best Local Similarity: 98.81% Mismatches: 4
Query Match: 97.71% Indels: 2
DB: 10 Gaps: 1

US-09-687-230a-2 (1-589) X US-09-764-864-792 (1-7053)

QY 3 Lysleuylslyblybshlybserasplybshileutyrgluglutyrglvalglulyspro 22
DB 208 AAGAAAGACAAAGACCAAGTCGACCAACCTCTACGAGGATATGAGAAAGCCC 267
QY 23 Leuylsleuvalleuylsvalgllyglsanglvalthrghlueusertthgliser 42
DB 268 TTGAAGCTGCTCTCAAGTATGAGGAGMCAAGTCCAGAACTCTCCAGGAGCTCG 327
QY 43 Glyhisaspserserleuphegluasplysasnashisaplybshlybasparglys 62
DB 328 GGGCAGACCTCCAGCTCTTGAGAGCAAAAACGATCATGCAAAACAGAGACAGAAAG 387
QY 63 Arglylsylsarglyblybgllyglulysglulileprogllyglulyslyarglyarg 82
DB 388 CGGAAAAAGAGAAAGAAAGAGAGAGAGATTCAGGGGAAAGAAAGGGGAGAAACGG 447
QY 83 Argargvallybgllyuasplyblyblybargbapargbapargvalgluasnglualglu 102
DB 448 AAGAGAGTTAAAGGAGTAAAGAAAGAGAGATCGAGCCGGGAGAGATGAGAGAGAA 507
QY 103 Lysaspheuglncysbshsalaaprovalargleuaspleuproprogllylproleuthr 122
DB 508 AAAGATCTCCAGCTCCAGCCCTCTGAGATTAGCTTGCTCCAGAAAGCTCTCA 567
QY 123 Serseerleualalybglnglulvalglulthrproleuglglualaleuasngl 142
DB 568 AGCTCTTACGCAAAAGAAAGAGAGATGAGACACCCCTTCAAGAGCTTTAAATCAA 627
QY 143 Leuuecarggluueuglnarglybaspserasaphepserpheprovalthr 162
DB 628 CTGATGAGACATTCGAGAGAAAGATCCAGTCTTCTTCACTTCTCTGATCGAT 687
QY 163 Pheilealaprogllytyrsermetilelybshispromeasaphepserthmetlys 182
DB 688 TTTATTCCTCTGCTCATCTCATGATCATTAACACCAATGATTTTAAAGCATGAAA 747
QY 183 Glulyslilelysasnashaptyrglinsertileglululeuylsaspasphenlyb 202
DB 748 GAAAGATCAAGAAATGATCATGATCCATAGAGAACTAAAGATTAACCTCAAACTA 807
QY 203 Metcysrthrashalameciletyrasnlybproglunthriletyrtyrlybalaalys 222
DB 808 ATGTGTACTAATGCGCATTTTACATTAACCAAGACCATTTATTAAGCTGCAAG 867
QY 223 Lysleuuehshiserglymetlysileuuserglnlualrglileglnserleuyls 242
DB 868 AAGCTGTTGCACTCAGAGATGAAAATTTCTTAGCCAGAGAAATTCAGAGCTGAAGAG 927
QY 243 Serileasphenmetalaaspleuglulysrthrlyrglybglulysapgllythr 262
DB 928 AGCATAGCTTCATGAGCTGATCTGACAGAAAACGAAAGATGAGAAAGACAGACC 987
QY 263 Serghlsergylgluasrglygllycysrthrlyrglunargllyuaspsrglyasp 282
DB 988 TCACAGAGTGGGAGAGAGAGAGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1047
QY 283 Glualahisalapelyserserproserlysglulasnlyblyblybaspaspleu 302
DB 1048 GAAACACACGCTCTCAAGAGTCCAGAGCAAGAAATTAAGAAAGAAAGAAAGATATGCTT 1107
QY 303 Gluasplybphenlybserasnashleuylunarglglnglulglulnleuaspar 322
DB 1108 GAAGATTAAGTTTAAAGCAATTAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1167
QY 323 Lysgluusergylgllyblyblybthrargargleuvalaenserglncysgluphegluarg 342

DB 1168 AAGAAATCTGAGAGAAAGCTGACACAGCGGCTGTGAAACATGATCGAATTTGAAAGA 1227
QY 343 Arglybproaspgllythrthrleuylleuuehshiprovalasproilleva 362
DB 1228 AGAAACCAAGATGAAACAAAGAGCTGGAGCTTCTCATCTGATGATTCATGATGAGA 1287
QY 363 Gluproglytyrtyrcysleuvalargleuylmetthrthrlybargleuglinsergly 382
DB 1288 GAGCAGGCTTACCTGCTGAGACTGGAGATGCACTGAAAGACTTCACTGAGTGGAGTG 1347
QY 383 Asnthrleuglnclybphenlysgluasplysargasnashlybthrprovalleuylleu 402
DB 1348 AATATCTTGACGGGTTCAAGAGAGATTAAGAAACAAATCTCACTCAAGTATATTTG 1407
QY 403 Asntrglyprotyrserserlyralaprohietyraspsertthpheaalasn 422
DB 1408 AATTATGGCCCTTACAGTTCTTATGACACCCCATATATCACTCATTTGCAAAATATCAGC 1467
QY 423 Lysaspaspserserleuiletyrserthrtyrlygluluaspserserleuproserasp 442
DB 1468 AAGATGATTTGATTTTAATCTTATCACTATGGGAGAACTTGATCTTCAAGTAT 1527
QY 443 PheSerilehsglupheleualathrcysglinsaptyrprotyrvalmetalaasps 462
DB 1528 TTGACATTCATAGATTTTGGCCAGCTGCAAGATTAATCGATGATGATGAGATAGT 1587
QY 463 Leuueasplalleuylthrlybgllybshisargthrleuglglumetglumetser 482
DB 1588 TTAATGATTTTAAACAAAGAGAGGATTCAGAGACCCCTTACAAAGATGAGATGATCA 1647
QY 483 Leuproglybapgllybshsthrargthrleuasphrghlybglumetglulile 502
DB 1648 TTGCTTAAAGTGAAGGCACTACTAGACACTTGACACAGCAAGAAATGAGAG-ATT 1704
QY 503 Thrghlualgluproproglyargleuaspserserthrghlinsapargleuilealeu 522
DB 1705 ACAGAAATAGACCAACAGAGGCGTTTGACCTCCAGTACTCAAGACAGGCTCATAGCGCTG 1764
QY 523 Lysalavalthrashpnegllyvalprovalglulvalpheaspserserglulualgluile 542
DB 1765 AAAGCAATTAACAAATTTGGCGTTCCAGTTGAAGTTTTCATCTGAAAGAGCTGAATA 1824
QY 543 Pheglulysleuuehshisapglunthrthrargleuuehshisapglnglualaglaasn 562
DB 1825 TTCAGAGAAAGCTTGAATGAGACCAACAGATGCTCGAGAACTCCAGAAAGCCAGAAAT 1884
QY 563 Gluaspleuserthrargproprogllyasnmetilecysleuueuglyproser-ser 582
DB 1885 GAAGCTTGAAGACACCAAGACCCCTCCGACATATCTGCTCTTGGGTCCCTCATACAGA 1944
QY 582 ulysCysileuuehshis 589
DB 1945 GAAATGCATCTTGCTGAACAAAG 1966

RESULT 2
US-09-764-864-379
; Sequence 379, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OR INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; PRIORITY FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 379
; LENGTH: 1351
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-864-379

APPLICANT: Wang, Jian-Rui
APPLICANT: Zhao, Qing A.
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: Wehrman, Tom
APPLICANT: Zhang, Jie
APPLICANT: Qian, Xiaohong B.
APPLICANT: Dimanac, Radoje T.
TITLE OF INVENTION: No. US20020197679A1e1 Nucleic Acids and
FILE REFERENCE: 784CIP2
CURRENT APPLICATION NUMBER: US/10/098,841
PRIORITY FILING DATE: 2002-03-13
PRIORITY FILING DATE: 2000-06-20
PRIORITY FILING DATE: 2000-06-20
PRIORITY FILING DATE: 2000-04-25
PRIORITY FILING DATE: 2000-04-25
PRIORITY FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 331
SOFTWARE: pc_fl_genes version 1.0
SEQ ID NO 196
LENGTH: 2830
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (110)..(1903)
US-10-098-841-196

Alignment Scores:
Pred. No.: 1,03e-83 Length: 2830
Score: 921.50 Matches: 213
Percent Similarity: 55.46% Conservative: 127
Best Local Similarity: 34.75% Mismatches: 184
Query Match: 29.99% Indels: 89
DB: 13 Gaps: 17

US-09-687-230A-2 (1-589) x US-10-098-841-196 (1-2830)

QY 1 MetGlyLysLysHisLysLysSerAsp---LysHisLeuTyrGluGluTyr--- 18
DB 110 ATGGGCAAGAGCAAGAGAGCAAGAGCCAGCGGCGCTCTCTACAGAGATTATGCC 169
QY 19 -----ValGluLysProLeuLysLeuValLeuLysValGluLysAsnGluValThr 35
DB 170 GACAAGCCCTGGAGAGAGCTCTAAAGCTAGTCTGAAAGTCCGAGAGAGTGAAGTACT 229
QY 36 GluLeuSerThrGlySerSerGlyHisAspSerSerLeuPheGluAspLysAsnAspHis 55
DB 230 GAACCTCA-----GGATCCGGCCACGACTCCAGTTACTATGATGACAGGTCAAGCCAT 283
QY 56 -----AspLysHisLysAspAspArgLysLysLysLysLysLysLysLysLysLysLys 72
DB 284 GAGCGAGAGAGGCAAG 343
QY 73 ---LleProGluGluGluLysGlyArgLysArgArgValLysGluAspLysLysLys 91
DB 344 CATCTGGACGATGAGAA-----AGAGGAAGCGAAAGGAAGGAAGAGAGAGAGAG 394
QY 92 ArgAspArgAspArgValGluAsnGluLysLysLysLysLysLysLysLysLysLys 110
DB 395 CGAAGAGAGGAGCACTGGACACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 454
QY 111 ValArgLeuAspLeuProProGluLysProLeuThrSerSerLeuAlaLysGluGlu 130
DB 455 GTGGAGGGGAGCGCGCGCGAGATCGGCACTCGAGGTCGCGAGACACAGCCGAA 514
QY 131 ValGluGlnThrProLeuGlnGluLysLysLysLysLysLysLysLysLysLysLys 150
DB 515 AATGAGAGCACTATTCAGCAACTCTGGAACACTTCTCCGCGAGCTTCAGAGAAA 574

QY 151 AspProSerAlaPhePheSerPheProValThrAspPheIleAlaProGluTyrSerMet 170
DB 575 GATCCCATGAGATTTTTCCTTCTCTGTCAGGATGCAATTGCTCTGATATTCATAG 634
QY 171 IleIleLysHisProMetAspPheSerThrMetLysGluLysIleLysAsnAspAspTyr 190
DB 635 ATATATAACATCCCATGATTTTGGCACCATGAAAGCAAAATTTAGCTTAATGAATAC 694
QY 191 GluSerIleGluGluLysLysAspAsnPheLysLeuMetCysThrAsnAlaMetIleTyr 210
DB 695 AAGTCACTTCGGAATTTAAAGCAATTCAGCTGATGCTGATATATGCAATGACATAC 754
QY 211 AsnLysProGluLysIleTyrTyrLysAlaAlaLysLysLeuHisSerGluMetLys 230
DB 755 AATAGCCAGATATCCGATCTACAGATTCGAGAGAGATCTTCACGAGGCTTTAAG 814
QY 231 IleLeuSerGlnLysArgIle-----GlnSerLeuLysGlnSerIle 244
DB 815 ATGATGAGCAAAAGGAGAGCTTTTGGCAATGAAATACAGCTGTGAGAACTGTGC 874
QY 245 AspPheMetAlaAspLeuGlnLysThrArgLysGlnLysAspGluThrAspThrSerGln 264
DB 875 CCTGAAGTTGTACCACTACAA----- 895
QY 265 SerGluGluAspGluGlyCysTrpGluArgGluArgLysAspSerGluAspAlaGluAla 284
DB 895 ----- 895
QY 285 HisAlaPheLysSerProSerLysGluAsnLysLysLysAspLysAspMetLeuGluAsp 304
DB 896 -----GTAGAACTGCCAGAAATATCCAAAAGCGAGTAGAGAAATATACAGCTGC 946
QY 305 LysPheLys-----SerAsnAsnLeuGluArgGlu 314
DB 947 ATGTTTACGCTGAGAGGAATGCTGAGCTTGCAGCAAGTCCGAAAGAGACAGCTG 1006
QY 315 GlnGluGlnLeuAspArgIleValLysGluSerGluLysLysLeuThrArgArgLysVal 334
DB 1007 CTGGCGCTGGTGGAGACGAGCTGACAGAAAGCTCGGACAGATCAACGGTCTCTCCA 1066
QY 335 AsnSerGlnCysGluPheGluArgArgLysAspArgLysThrThrThrLeuGluLeu 354
DB 1067 GGGCGCAAGATGGCTATCTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1126
QY 355 HisProValAspProIleValGluLysProGluTyrCysLeuValAlaGluGluMetThr 374
DB 1127 AACACGGCCGAGCGGAGCGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1186
QY 375 ThrGluArgLeuGlnSerGluValAsnThrLeuGlnGluPheLysGluAspLysArgAsn 394
DB 1187 TCCAGTAACTATCTCCAGGCTTCCACAGCTG---GGCTTCAAGAGAGAGAGAGAG 1243
QY 395 LysValThrProValLeuTyrLysAsnTyrGlyProTyrSerSerTyrAlaProHisTyr 414
DB 1244 AAGTCACTC-----TTTCTCTCC---AGTGCACATGCTGGCTTGTGATGAGATC 1291
QY 415 AspSerThrPheAlaAsnIleSerLysAspAspSerAspLeuIleTyrSerThrTyrGly 434
DB 1292 AATTCAGTATTTGGCGACTTGAAGTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1351
QY 435 GluAspSerAspLeuProSerAspPheSerIleHisGluPheLeuAlaThrCysGluAsp 454
DB 1352 GATGAGACAGGCTGAGCTGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1411
QY 455 TyrProTyrValMetAlaAspSerLeuLeuAspValLeuThrLysGluLysHisSerArg 474
DB 1412 TACAGCAAGAAAGTGGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1471
QY 475 ThrLeuGlnLysLeuGlu-----MetSerLeuProGluAspGluGly 488
DB 1472 ACGCTTTCAGCTGAG 1531

QY 489 HieThraThrlieu---AspThrglyLyseGluMetGluGlnIleThrgluValGluPro 507
DB 1532 GTTGGGACACCTTAGAGAGACAGACAGCTCTGTTCTGAGTTTCATGTGATAG--- 1588
QY 508 ProGlyArgLeuApsSerSerThrglnApsArgLeuIleAlaValAlaValThraAsn 527
DB 1589 -----TCTATCCGACGTTTCTGTGATATCTCATCTCAGCTCT 1630
QY 528 PheGlyValProValGluValPheApsSerGluGluIlePheGlnIleValLeu 547
DB 1631 CTGGGGAAAGTGAAGAGAGCTGACCTGACAGACCACTTGG-----ACCTG 1661
QY 548 AspGluThraThraGluLeuArgGluLeuGlnIleAlaGlnApsArgLeuSerThr 567
DB 1682 GATGAGACGAGAGAGCTCTCTGACAGACCTGACAGAGACAGGGGCGGCGCTCT 1741
QY 568 ArgProProGlyApsMetIleCysLeuLeuGlyProSer 580
DB 1742 CGGCGCTGTCACACCTGCTCCCTGTCACACCTCTCC 1780

RESULT 4

US-09-677-701-2944
; Sequence 2944, Application US/09867701
; Patent No. US2002032237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2944
; LENGTH: 517
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(517)
; OTHER INFORMATION: n = A,T,C or G
US-09-677-701-2944

Alignment Scores:
Pred. No.: 9.52e-80 Length: 517
Score: 872.50 Matches: 170
Percent Similarity: 98.27% Conservative: 0
Best Local Similarity: 98.27% Mismatches: 2
Query Match: 28.39% Indels: 1
DB: 10 Gaps: 1

US-09-687-230a-2 (1-589) x US-09-677-701-2944 (1-517)

QY 377 ArgLeuGlnSerGlyValIleThraThraGluGlyPheGluApsArgLeuVal 396
DB 1 AGACTTAGTCTGAGAGAACTTCTGACGGCTTCAAGAGGATTAAGAACAAAGTC 60
QY 397 ThrProValLeuThraLeuApsArgLeuProThraIlePheSerThrglyGluAps 416
DB 61 ACTTCAGTGTATATTTGATATGAGCCCTTCAAGCTTATGACCGCATTTATGCTCC 120
QY 417 ThrPheAlaAsnIleSerLyApsApsSerApsLeuIleThraThraThrglyGluAps 436
DB 121 ACATTTCAATATACAGCAAGATGATTCGATTTATCTATTCACCTATGGGAGAC 180
QY 437 SerApsLeuProSerApsApsSerIleHisGluPheLeuAlaThraCysGlnApsThraPro 456
DB 181 TCTGATCTTCAAGTATTCATGATCATGAGTTTGGCCAGTGTCCAGATTTATCCG 240
QY 457 TyraValMetAlaApsSerLeuApsValLeuThraThraGlyHisSerArgThraLeu 476

DB 241 TATGTCAGCAGATGATTACTGATGTTTAAACAAAGAGGGCATCTCAGACCTTA 300
QY 477 GlnGluMetGluMetSerLeuProGluApsGluGlyHisThraThraThraApsThrgly 496
DB 301 CAGAGATGAGAGATGATTCCTGAGAGATGAAGGCCATATCTGAGACATTCACAGCA 360
QY 497 LyseGluMetGluGlnIleThrgluValGluProProGlyArgLeuApsSerThrgln 516
DB 361 AAGAAATGAG---ATTACAGAGTAGAGCCACAGGCGCTTGGACCTCAGACTCA 417
QY 517 AspArgLeuIleAlaLeuValAlaValThraPheGlyValProValGluValPheAps 536
DB 418 GACAGGCTCATACCGCTGAAGAGCATTAACAATTTGGCTTCAGTTGAAGTTTGGAC 477
QY 537 SerGluGluAlaGluIlePheGlnIleValLeuApsGlu 549
DB 478 TCTGAAGAGCTGAMATATTCAGAAAGAACTTGATGAG 516

RESULT 5

US-09-918-995-37236
; Sequence 37236, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 37236
; LENGTH: 480
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(480)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-37236

Alignment Scores:
Pred. No.: 2.35e-70 Length: 480
Score: 780.00 Matches: 153
Percent Similarity: 96.23% Conservative: 0
Best Local Similarity: 96.23% Mismatches: 6
Query Match: 25.38% Indels: 1
DB: 11 Gaps: 0

US-09-687-230a-2 (1-589) x US-09-918-995-37236 (1-480)

QY 284 AlaHisAlaPheApsSerProSerLyseGluApsLyseLyseApsApsMetLeuGlu 303
DB 3 GCACAGGCTTCTCG-AGTCCACAGCAAGAAATTAAGAAAGAAAGATATGCTTGA 61
QY 304 AspLysePheLyseSerApsApsLeuGluApsGluGlnIleLeuApsArgIleValys 323
DB 62 GATTAAGTTTAAAGCAATATTTATGAGAGAGACAGAGACGCTTGAACCGCATCGTGAAG 121
QY 324 GluSerGlyGlyLyseLeuThraGluValAlaAsnSerGlnCysGluPheGluApsArg 343
DB 122 GAATTCGAGGAGAAAGCTGACAGCGCGCTTGTAAAGTCAGTCAGCAATTTGAAGAGA 181
QY 344 LyseProApsGlyThraThraThraGluLeuHisProValApsProIleValGlyGlu 363
DB 182 AAACCGAGTAGAACAGACAGCTTTCATCTCTGATCCATTTGAGAGAG 241
QY 364 ProGlyTyraCysLeuValArgLeuGlyMetThraThraGlyArgLeuGlnSerGlyValAsn 383
DB 242 CCAAGCTACTGCGCTGTGAGACTGGAGATGACAACTGAAAGAACTTCAGTCTGAGTGAAT 301

Qy 384 ThrLeuGlnGlyPheLeuAspLeuArgAsnValThrProValLeuThrLeuAsn 403
Db 302 ACTTGACAGGGCTTCANAGAGATAAAGAAAGAAAGCTTCCAGCGTTATTTGAT 361
Qy 404 TyGlyProTyrSerSerTyrAlaProHisTyrAspSerThrPheAlaAsnHisSerLys 423
Db 362 TATGGGCGCTCAGATTCTTATGACACCGCATATATCATCTCCATTTGCAAAATATCAGCAG 421
Qy 424 AspAspSerAspLeuLeuTyrSerThrTyrGlyGluAspSerAspLeuProSerAsp 442
Db 422 GATGATTCGTGATTAACTTATTTCAACCTATGGGAGAGCTGTGATCTTCAAGTAT 478
RESULT 6
US-09-960-352-7102
Sequence 7102 Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengping
APPLICANT: Byatt, John C.
APPLICANT: Mathiasen, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 7102
LENGTH: 421
TYPE: DNA
ORGANISM: Bos taurus
FEATURE:
NAME/KEY: unsure
LOCATION: (115)
OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: 31-BOWMS1-003-Q1-E1-H3
US-09-960-352-7102
Alignment Scores:
Pred. No.: 4,02e-42 Length: 421
Score: 502.50 Matches: 106
Percent Similarity: 85.61% Conservative: 7
Best Local Similarity: 80.30% Mismatches: 17
Query Match: 16.35% Indels: 2
DB: 10 Gaps: 1
US-09-687-230A-2 (1-589) x US-09-960-352-7102 (1-421)
Qy 459 MetAlaAspSerLeuLeuAspValLeuThrLysGlyGlyHisSerArgThrLeuGln 478
Db 1 ATGGAAGTACTTTCATCTGATGATGTTTAAACAAAAGAGAGCTTCCAGAACCTTCAGAG 60
Qy 479 MetGluMetSerLeuProGluAspGluGlyHisThrArgThrLeuAspThrGlyLysGlu 498
Db 61 TCAGAGACGTCATCTCCGAGAGATGAGGCGCAGACTAGATTAATTGACACAGCANAAAGAA 120
Qy 499 MetGluGlnLeuThrGluValGluProProGlyArgLeuAspSerSerThrGlnAspArg 518
Db 121 ATGAG---GTTACAGAAAGTTGAACCTAACAGATGTTGACTCCAAATATCAAGACAG 177
Qy 519 LeuLeuAlaLeuLysAlaValThrAspNheGlyValProValGluValPheAspSerGlu 538
Db 178 CTTACAGACACTGAAGACGTAACAACTTCGAGCTCCGTTGAAAGTTTGGACTTCGAA 237
Qy 539 GluAlaGluLeuPheGlnLysLysLeuAspGluThrThrArgLeuLeuArgGluLeuGln 558
Db 238 GAACTGAAGTCTCCAGAGAACTTGATGACACCAAACTGCTCAGAGAGCTCAG 297
Qy 559 GluAlaGlnAsnGluGluSerThrArgProProGlyAsnMetLysCysLeuLeuGly 578
Db 298 GAAACCCAGATGAGCGCTGAGCACGACCCCTCTCAACATGATCTGTCTTGGGT 357
Qy 579 ProSer-SerLysCysLysLeuLeuAsnLys 589

Db 358 CCGTCATACAGAGAAATGATCTTGCTGAGACAG 391
RESULT 7
US-09-960-253-96
Sequence 96 Application US/09960253
Patent No. US20020123619A1
GENERAL INFORMATION:
APPLICANT: Benson, Darin R.
APPLICANT: Mohamed, Radoh
APPLICANT: Lodes, Michael J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.556
CURRENT FILING DATE: 2001-09-20
NUMBER OF SEQ ID NOS: 197
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 96
LENGTH: 513
TYPE: DNA
ORGANISM: Homo sapiens
US-09-960-253-96
Alignment Scores:
Pred. No.: 2.12e-39 Length: 513
Score: 477.00 Matches: 89
Percent Similarity: 71.68% Conservative: 35
Best Local Similarity: 51.45% Mismatches: 45
Query Match: 15.52% Indels: 4
DB: 10 Gaps: 2
US-09-687-230A-2 (1-589) x US-09-960-253-96 (1-513)
Qy 64 LysLeuArgLysLysGlyGlyGlnLeuProGlyGluGluLysGlyArgArg 83
Db 3 AAGAGAAAGTCCAGAGAGAGAAAGCATCTGACGATGAGAA-----AGAAAGAG 53
Qy 84 ArgValLeuGluAspLysLysArgAspArgAspArgValGluAsnGluValGlu 102
Db 54 CGAAGGAAAGAAAGAAAGCGAAGCGAGAGAGAGACGTGTGACAGAGAGAGAGCT 113
Qy 103 LysAspLeuGlnCysHisAlaProValArgLeuAspLeuProProGlyLysProLeuThr 122
Db 114 GACGACTTATCTCGGAGAGAGAGTGTGAGTGTGAGCGGCCCGCCAGATCGCGTCGA 173
Qy 123 SerSerLeuAlaLysGlnGluValGluGlnThrProLeuGlnGluAlaLeuAsnGln 142
Db 174 GCGTCCGACACAGACCGCCGAAATGAGAGCACCTTTCAGCAACTCTCGAACAC 233
Qy 143 LeuMetArgGlnLeuGlnArgLysAspProSerAlaPhePheSerPheProValThrAsp 162
Db 234 TTCCTCCGAGCTTCAGAAAGATCCCATGATTTTGTCTTCTGTCACGAT 293
Qy 163 PheLeuAlaProGlyTyrSerMetLeuLeuHisIlePheMetAspPheSerThrMetLys 182
Db 294 GCAATTCCTCTGATTTTCAATGATATATAAATCATTCATGATTTTGGCACCATGAAA 353
Qy 183 GluLysIleLysAsnAsnAspTyrGlnSerIleGluGluLeuLysAspAsnPheLysLeu 202
Db 354 GACAAATTTAGCTATATGATATCAATCAAGTCAAGAAATTAAGCAATTTCAAGCTG 413
Qy 203 MetCysThrAsnAlaMetIleTyrAsnLysProGluThrThrLysTyrLysAlaLys 222
Db 414 ATGTGATATATGAAAGACATCAATAGCGCAGATACCGTGTACTCAAGTTGGCGAAG 473
Qy 223 LysLeuLeuHisSerGlyMetLysIleLeuSerGlnLys 235
Db 474 AAGATCTTCAACGAGGCTTAAAGATGATGAGCAAAACAG 512
RESULT 8
US-09-764-864-792/C
Sequence 792 Application US/09764864

Patent No. US20020132753A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT223
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1792
SOFTWARE: Patentn Ver. 2.0
SEQ ID NO 792
LENGTH: 7053
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (154)
OTHER INFORMATION: n equals a,t,g, or c
US-09-764-864-792

Alignment Scores:
Pred. No.: 9 11e-26 Length: 7053
Score: 359.00 Matches: 68
Percent Similarity: 94.52% Conservative: 1
Best Local Similarity: 93.15% Mismatches: 4
Query Match: 11.68% Indels: 0
DB: 10 Gaps: 0

US-09-687-230A-2 (1-589) x US-09-764-864-792 (1-7053)

Qy 246 PheMetAlaSpLeuGlnLysThrArgLysGlnLysAspGlyThrAspThrSerGlnSer 265

Db 221 TTCTGTGCTTCTTGCAGAAACCTCGAAGAGAAATGGAACAGACCTCCACAGT 162

Qy 266 GlyGlnAspGlyGlyCysTrpGlnArgGlnArgGlnAspSerGlyAspAlaGlnAlaHis 285

Db 161 GGGGAGGCGGAGGCTCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 102

Qy 286 AlaPheLysSerProSerLysGlnAsnLysLysLysLysLysLysLysLysLysLysLys 305

Db 101 GCCTTCAGAGTCCCGACCAAGAAATPAAAAAGAAAGCAAGATGCTTGAAGATAG 42

Qy 306 PheLysSerAsnAsnLeuGlnArgGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 318

Db 41 TTTAAAGCAATATTTAG 3

RESULT 9
US-10-096-534-53
Sequence 53, Application US/10096534
Publication No. US20030166887A1

GENERAL INFORMATION:
APPLICANT: The Brigham and Women's Hospital, Inc.
APPLICANT: Yates, Karen
APPLICANT: Mizuno, Shunichi
APPLICANT: Glowacki, Julie
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF SKELETAL DEGENERATION CONDITIONS
FILE REFERENCE: B0801/7244/KA/ERP
CURRENT APPLICATION NUMBER: US/10/096,534
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: US 60/274,980
PRIOR FILING DATE: 2001-03-12
NUMBER OF SEQ ID NOS: 79
SOFTWARE: Patentn version 3.0
SEQ ID NO 53
LENGTH: 1861
TYPE: DNA
ORGANISM: Homo sapiens
US-10-096-534-53

Alignment Scores:
Pred. No.: 6.63e-18 Length: 1861
Score: 274.00 Matches: 79
Percent Similarity: 48.53% Conservative: 70

Best Local Similarity: 25.73% Mismatches: 126
Query Match: 8.92% Indels: 32
DB: 12 Gaps: 8

US-09-687-230A-2 (1-589) x US-10-096-534-53 (1-1861)

Qy 291 SerLysGlnAsnLysLysLysLysAspLysAspMetLeuGlnAspLysPheLys----- 307

Db 94 GCCAAGAAATCCAAAAGCCGAGTACAGAGATTATACAGCTGCATGTTTGAAGCCCGAAGG 153

Qy 308 -----SerAsnAsnLeuGlnArgGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 320

Db 154 AATGCTTCAGCTTTCAGGACGAGATACCGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 213

Qy 321 IleValIleGlnSerGlyGlyLysLeuThrArgArgLeuValAsnSerGlnCysGlnPhe 340

Db 214 GCAGCTGACGAGCTCGGACAGATCAACCGGTTCTCCAGCGGCAAGATGGCTAT 273

Qy 341 GlnArgArgLysProAspGlyThrThrThrLeuGlyLeuLeuHisProValAspProIle 360

Db 274 CTGAAGAGAAACGGGACCGGAGCTCTGCTACAGCTGTGTCACACCGCCGAGCCGAG 333

Qy 361 ValGlyGlnProGlyTyrCysLeuValArgLeuGlyMetThrThrGlyArgLeuGlnSer 380

Db 334 GTGATGAG 393

Qy 381 GlyValAsnThrLeuGlnGlyPheLysGlnAspLysLeuValThrProValLeu 400

Db 394 GGCTTCACCGCTG---GGCTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 441

Qy 401 TyrLeuAsnTyrGlyProLysSerSerTyrAlaProHisTyrAspSerThrPheAlaAsn 420

Db 442 TTCTCTCC---AGTGCCACTACTGCGCTTTCATGACAGATATATTCAGATTGGGAC 498

Qy 421 IleSerLysAspAspSerAspLeuIleTyrSerThrTyrGlyGlnAspSerAspLeuPro 440

Db 499 TTGAAGTCGAGAGAGATGAG 558

Qy 441 SerAspPheSerIleHisGlnPheLeuAlaThrCysGlnAspTyrProTyrValMetAla 460

Db 559 TGTGCGCTGAGCTCGAG 618

Qy 461 AspSerLeuAspValLeuThrLysGlyGlyHisSerArgThrLeuGlnGlnMetGlu 480

Db 619 GACGACCTCTGAGACAGATCACAGCGGAGAGACACTTGGAGCGCTTCCAGCTAG 678

Qy 481 -----MetSerLeuProGlnAspGlnGlyHisThrArgThrLeu--- 493

Db 679 CAGAGAAATGTTCCATGAAGCTCCAGATGAAGCCAAAGTTGGGAGACCTTAGA 738

Qy 494 AspThrGlyLysGlnMetGlnGlnIleThrGlnValGlnProProGlyArgLeuAspSer 513

Db 739 GACGAGAGAGCTCTGTTGAGGTTCAATCATAGAG----- 777

Qy 514 SerThrGlnAspArgLeuIleAlaLeuLysAlaValThrAsnPheGlyValProValGlu 533

Db 778 TCTTATCCGACCTTCTGTGATATCTCATGCTCTGCGAAGGTGAAGAG 837

Qy 534 ValPheAspSerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 553

Db 838 GAGCTGAGCCCTGACAGACAGCACTTGG-----AAGTTGATGAGAGAGAGAGCTC 888

Qy 554 LeuArgGlnLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 573

Db 889 CTGAGAGAGCTGACAG 948

Qy 574 IleCysLeuLeuGlyProSer 580

Db 949 AGCTCCCTGTCACAGCGCTTC 969

RESULT 10
US-10-037-270-266
Sequence 266, Application US/10037270

```
Publication No. US20030104529A1
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Aseundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yungding
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: Tillinghast, John
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20030104529A1el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP28
CURRENT APPLICATION NUMBER: US/10/037, 270
CURRENT FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1104
SOFTWARE: pc Fl_genes Version 1.0
SEQ ID NO 266
LENGTH: 4549
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (186)..(3362)
US-10-037-270-266

Alignment Scores:
Pred. No.: 8,84e-16 Length: 4549
Score: 258.50 Matches: 109
Percent Similarity: 23.85% Conservative: 62
Best Local Similarity: 23.49% Mismatches: 136
Query Match: 8.41% Indels: 157
DB: 14 Gaps: 15

US-09-687-230A-2 (1-589) x US-10-037-270-266 (1-4549)
QY 11 AsprylhlsleuTYrglgluTY:ValglulysProleuLYleuValleuLYsValglY 30
DB 1341 GATGTCCACAGCCTCCAGGCTGCACCCGGAGCCTCTGAATATTATTCAGGGAGTTC--- 1397
QY 31 GlYsngluValThrglLeuSerThrglYserSerglYhlsAspSerSerleuPheglu 50
DB 1398 -----GAAATGAAAAATGCGCTCTGTGAAAAAGAGAGCTCGTTAAAAAG 1442
QY 51 AsrlyshsnaAsrhlshAsrlyshlsYsAsrlyshlYsValglYsValglYglu 70
DB 1443 GTCCAGTCC-----ACATCCAAAGGTCAAGAAAGGCAAAAAAGGCTAAG 1487
QY 71 Lys-----GlnlleProglY 75
DB 1488 AAACCTGTGCTGAGCCCTGCGCGGTCTCTCCGACCGGTGCGCTCTTATATTCGCCCG 1547
QY 76 GlulglulysglYsArglyshArglyshValglYsValglYsValglYs 91
DB 1548 CAGAGCTTAATATGATTCGCAATCAGGTGSCCATTCACGGGAAGACACTTTGTGAG 1607
QY 91 ----- 91
DB 1608 CGAGCCACAGCTACTGCTGCTCAAGCGGCTGTCCAGAAAGGGGCCCTCTGCTGCGG 1667
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QY 92 -----ArgshAsrAsrArgVal 97
DB 1668 CGGCTGACAGTCCAGCTGACGTCTCAAGCAAGCTCACAGACAGAGAAAATGATGAGAG 1727
QY 98 GluAsngluAglulysAsrleuGlncYshlsAlProValArgleuAsrleuProPro 117
DB 1728 ATGAAGCTGCCAAAGAGAAAGTGAAGTCTGGACCGCTGCGGACGACTGAGCCG 1787
QY 118 GlulysProleuThrsSerSerleuAllysGlulY-----Glu 130
DB 1788 GCTCGCTGCTGTATCGAGCTGTGCGCCAGCGGGAAGCTCAAGCTGACAGGTGAG 1847
QY 131 ValGluln-----ThrProleuGlulAlaueAsnglu 143
DB 1848 GTGAGACAGGTCCCATGAGCTGCGGCTGACCCCGCTGACGCTGCTGCTGCTCAGTG 1907
QY 144 MetArgGlulnGlulnArglyshAsrProserAlshPhePheSerPheProValThrsPhe 163
DB 1908 CTGAGCCAGCTGCMAAGCAAGAGACCCCGCAGAGATTTGGCAGCCCGTGAAGCTGAG 1967
QY 164 lleAlaProglYTrsMetllelYshlsPProMetAsrPheSerThrsMetlyglu 183
DB 1968 GAGGTACCAATTAATTTGATCAATTAACATCCCATGAGCTTTGCCAATAGAGAAA 2027
QY 184 LyslleYshsnaAsrPYrglnSerlleglulYleuLYsAsrshAsrPheLYsMet 203
DB 2028 CGGTTGAAGCTCAAGGATTAATAAACTCCATGAGATTGAGAGAGATTGATTCATTCAT 2087
QY 204 CysThrsAlaMetlleYshlsPProglulThrlYTrYshlsAlaAllys 223
DB 2088 ATGATTAACCTGATGAATGAATGCAATGCGAGGACCGGTGTTATGAGCGCGGTGAGG 2147
QY 224 LeuLeuHisSerglYmetlyshleuSerglulnArglleGlnSerleuLYsGlnSer 243
DB 2148 CTGCGCATCAGAGAGGTGTGTTCTGAGCAGAGCCCGG----- 2186
QY 244 llsAsrPheMetAlaAsrleuGlulYshArglyshlYsAsrglYThrsPThrsSer 263
DB 2186 ----- 2186
QY 264 GlnSerlygluAsrlyglYCystrPglnArggluArggluAsrSerlyshAsrAlaGl 283
DB 2187 -----CGGAGGTGAGACAGATCGGCTTGAAAGAG 2216
QY 284 Ala-----HisAlaPheLYsSerProserlyglulnAsrLYs 296
DB 2217 GCTTCGGGAGTCACTGCTGCTGAGCGGCTGTCTGCGGACCGCGGCGCTTCTCTG 2276
QY 297 LysAsrlyshAsrMetleuGlulAsrlyshPheLYsSerAsrshAsrleu-----GluArg 313
DB 2277 GAAGAGGTGACAGAGTGTGAGACCCCGCAACAGACCCACTGTGGGCTGAGAGAGACAG 2316
QY 314 GlulnGlulnleuAsrArglle-----VallysglYserglYglYs 328
DB 2337 CTGAGAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2396
QY 329 LeuThrsArg-----ArgleuValAsrSerGlnCysglulPheglulnArglyshProAsr 347
DB 2397 AGCAAGCGGCAAGAGCTGCTCAAAAAGAAATTCCTTCTCCGAAACAAAG----- 2447
QY 348 ThrThrsThrsleuGlulnleuHisPProValAsrProlleValglYglulnProglYTrsCys 367
DB 2448 -----CTGAGCCAGCAGACAGC-----CAGCCCTGCCACAGGGGCCAGGC----- 2489
QY 368 LeuValArgleuGlulnMetThrsArgleuGlnSerlyshValAsrThrsleuGlnGlY 387
DB 2490 -----TTGGAAGGC 2498
QY 388 PheLYsGlulnAsr 391
DB 2499 TTCGAAGAGGAC 2510
RESULT 11
```


US-10-037-270-267
 ; Sequence 267, Application US/10037270
 ; Publication No. US20030104529A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tang, Y. Tom
 ; APPLICANT: Liu, Chenghua
 ; APPLICANT: Asundi, Vinod
 ; APPLICANT: Zhang, Jie
 ; APPLICANT: Ren, Feiyan
 ; APPLICANT: Chen, Rui-hong
 ; APPLICANT: Zhao, Qing A.
 ; APPLICANT: Weinman, Tom
 ; APPLICANT: Xue, Aidong J.
 ; APPLICANT: Yang, Yonghong
 ; APPLICANT: Wang, Jian-Rui
 ; APPLICANT: Zhou, Ping
 ; APPLICANT: Ma, Yundong
 ; APPLICANT: Wang, Dunrui
 ; APPLICANT: Wang, Zhilwei
 ; APPLICANT: Tillinghast, John
 ; APPLICANT: Drmanac, Radoje T.
 ; TITLE OF INVENTION: No. US20030104529A1el Nucleic Acids and
 ; TITLE OF INVENTION: Polypeptides
 ; FILE REFERENCE: 784CIP2B
 ; CURRENT APPLICATION NUMBER: US/10/037, 270
 ; CURRENT FILING DATE: 2002-01-04
 ; PRIOR APPLICATION NUMBER: 09/552,317
 ; PRIOR FILING DATE: 2000-04-25
 ; PRIOR APPLICATION NUMBER: 09/488,725
 ; PRIOR FILING DATE: 2000-01-21
 ; NUMBER OF SEQ ID NOS: 1104
 ; SOFTWARE: PL FL_genes, Version 1.0
 ; SEQ ID NO 267
 ; LENGTH: 4942
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (186)..(3755)
 ; US-10-037-270-267

Alignment Scores:
 Pred. No.: 9,93e-16 Length: 4942
 Score: 258.50 Matches: 109
 Percent Similarity: 36.85% Conservative: 62
 Best Local Similarity: 23.49% Mismatches: 136
 Query Match: 8.41% Indels: 157
 DB: Gaps: 15

US-09-687-230A-2 (1-589) x US-10-037-270-267 (1-4942)

QY 11 AsplyshisleutyrgluGluTVaIGluysProleuLysLeuValLeuLysValIGly 30
 DB 1341 GATGTTCACGCGCTCCAGCGTGACCCGAGCGCTCTGAATATTTCAGGGAGTGC--- 1397
 QY 31 GlyAsnGluValThrgluLeuSerThrglySerSerGlyHisAspSerSerLeuPhgGlu 50
 DB 1398 -----GAAATGAAATAATGGCGTCTGTGAAAGAGAGCTCGTTAAACG 1442
 QY 51 AsplyshAspHisAspLysHisLysAspArgLysLysLysLysLysLysLysLysLys 70
 DB 1443 GTCAAGTCC-----ACATCCAGGTCAAGAAAGAGCAAAAAGGCTTAAG 1487
 QY 71 Lys-----GlnIleProGly 75
 DB 1488 AAGAGCTGTGCTGAGCCCTGCGCGCTCTGCGCAAGCTGTGCGCTTATTCCTCCCG 1547
 QY 76 GluGluLysGlyArgLysArgArgValLysGluAspLysLysLys----- 91
 DB 1548 CAGAGGTTAAATAGAGATTGCCAATCAAGTGGCCATTCAAGCGAAGAGAGCTTTGGAG 1607
 QY 91 ----- 91

DB 1608 CGAGCCACAGTACTGCTGCTCAACGGGCTGTCCAGAAAGGAGCCCTCTGCTCGG 1667
 QY 92 -----ArgAspArgAspArgVal 97
 DB 1668 CGGCTGAGTTCAGCTTCAGCTTCAGCGAAGCTCACAGCAAGAAATGAGAGAG 1727
 QY 98 GluAsnGluValGluLysAspLeuGlnCysHisIleAlaProValArgLeuAspLeuProPro 117
 DB 1728 ATGAAGGCTCCAAAGAAAGAGCTGAATCTGGAGAGGCGCTGGCCAGCTGGAGCCG 1787
 QY 118 GluLysProLeuThrSerSerLeuAlaLysGlnGlu-----Glu 130
 DB 1788 GCTCGCTGCTGATCCAGCTGCTGCCAGCGGAGAAAGCTCAAGCTGAGAGAGTGAAG 1847
 QY 131 ValGlnGln-----ThrProLeuGlnGluAlaLeuAsnGln 143
 DB 1848 GTGAGAGAGTCCGATGAGAGCTGCGGCTGACCCCGTGAACGCTGCTGCGCTCAGTG 1907
 QY 144 MetArgGlnLeuGlnArgLysAspProSerAlaPhePheSerPheProValThrAspPhe 163
 DB 1908 CTGAGCCAGCTGCAGAGCAAGAGACCCGCAAGATATTTCGCGAGCCCTGAGCTGAAG 1967
 QY 164 IleAlaProGlyTyrSerMetIleIleLysHisProMetAspPheSerThrMetLysGlu 183
 DB 1968 GAGGTACCAAGATTATTGATCATCATTAACATCCCATGAGCTTGCCACAAATGAGGAAA 2027
 QY 184 LysIleLysAsnAspLysArgLysLysLysLysLysLysLysLysLysLysLysLys 203
 DB 2028 CGGTTAAGAGCTCAAGGAGTTAAACCTTCATGATGATGAGAGAGATTTTGATTCATT 2087
 QY 204 CysThrAsnAlaMetIleTyrAsnLysProGluThrIleTyrTyrLysAlaAlaLysLys 223
 DB 2088 ATGATATACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2147
 QY 224 LeuLeuHisSerGlyMetLysIleLeuSerGlnGluArgGlnIleGlnSerLeuLysSer 243
 DB 2148 CTCGCGCATCAGAGAGGATGTTGTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2186
 QY 244 IleAspPheMetAlaAspLeuGlnLysThrArgLysGlnLysAspGlyThrAspThrSer 263
 DB 2186 ----- 2186
 QY 264 GlnSerGlyGluAspGlyGlyCysTrpGlnArgGluArgLysAspSerGlyAspAlaGlu 283
 DB 2187 -----CGGAGGTGACAGCATCGGCTTGGAAAG 2216
 QY 284 Ala-----HisAlaPheLysSerProSerLysGluAsnLysLys----- 296
 DB 2217 GCCTCGGCGATGACCTGCTGAGCGGCGCTGTCGCGGACCGGCGGCGCTTCTCTCG 2276
 QY 297 LysAspLysAspMetLeuGluAspLysPheLysSerAsnAsnLeu-----GluArg 313
 DB 2277 GAAGACGTGACAGGTTGCTGAGACCCCGCAAGAGCCACCTGGCGCTGAGAGAGCAG 2336
 QY 314 GluGlnGlnGlnLeuAspArgIle-----ValLysGlnSerGlyLysLys 328
 DB 2337 CTGAGAGAGCTGTGAGCATGCTGACCTGACCTGACCTGAGCTGATGAAGTCCAGGCTCC 2396
 QY 329 LeuThrArg-----ArgLeuValAsnSerGlnCysGluPheGlnArgLysProAspGly 347
 DB 2397 AGCAAGCGGCAAGAGCTGCTCAAAAGAAATGGCTTCTCGAAACAG----- 2447
 QY 348 ThrThrThrLeuGlnLeuLeuHisProValAspProLysValGlyLysProGlyTyrCys 367
 DB 2448 -----CTGAGCCAGAGCAGCAGC-----CAGCCCTGCGCAAGGAGGAGGAGG 2489
 QY 368 LeuValArgLeuLysMetThrThrArgLysLeuGlnSerGlyValAsnThrLeuGlnGly 387
 DB 2490 -----TTGGAAGGC 2498
 QY 388 PheLysGluAsp 391
 DB 2499 TTCGAAGAGAGC 2510

Db 5127 ATTCAATTTCTCCGCCCACTGTCCTCCGACACCGCTTTACATGAGA---TCCTTATT 5183
Qy 464 UASpval-----LeuThlysglygllyhiseraThrle 476
Db 5184 GGAATATTAGATGTGAGAGAAATTAGGATATGACAGGGCACATCTGGGCTGTCT 5243
Qy 476 UGInglumecglumetserleuprogluaspgluylhis 489
Db 5244 CCAAGTAGAGAGATGATTACATCTTCATTCGACACCACTGATCAAAAATACCCAG 5303
Qy 490 -----ThrrgThrleuaspThrglyly 497
Db 5304 CCAAAACGACTGACAGAGTGTACAAAAGATCTGACAAAGCGCTTGACAGCGGATC 5363
Qy 497 sgIumecglu-GlnIleThrgluValGluProProgllyArgleuaspSer-Thrgln 516
Db 5364 ATCCATGACTACAA-----GGAATATTTTCAAAACAAAGCAACTGAA 5402
Qy 517 AspArgleuIleAlaLeuLysAlaValThrAspPheglYValProValGluValPheasp 536
Db 5403 GACAGCTCACCACTGCGCAAGAACTGCCCTATT----- 5438
Qy 537 SerGluLysAlaGluIlePheGlnLysLysLeuaspGluThrThrArgleuLysArgGlu 556
Db 5439 -----GAGGTGATTTCTGGCCCAATGTGTAGAGAGAGC-----ATTAAGAA 5483
Qy 557 LeuGlnLysAlaGlnAsnGluArg 564
Db 5484 CTAGAACAGAAAGAGAGAGAGG 5507

RESULT 13
US-09-925-301-104
; Sequence 104, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 104
; LENGTH: 1636
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-301-104

Alignment Scores:
Pred. No.: 2,01e-12 Length: 1636
Score: 219.50 Matches: 75
Percent Similarity: 48.30% Conservative: 53
Best Local Similarity: 28.30% Mismatches: 94
Query Match: 7.14% Indels: 44
DB: 9 Gaps: 11

US-09-687-230A-2 (1-589) x US-09-925-301-104 (1-1636)

Qy 323 LysGluSerGlyLysLeuThrArgArgLeuValAsnSerGlnCysGluPheGluArg 342
Db 40 GAGAGCGGACGCGAGCGCTGCTCTACAGCGTGTCAACAGCGCC-----GAGCGA 90
Qy 343 ArgLysProaspGlyThrThrThrLeuGlyLeuLeuHisProValAspProIleValGly 362
Db 91 CGCGATGAGAGAGA-----GACCA----- 111
Qy 363 GluProGlyTyrcysLeuValArgLeuGlyMetThrThrglyArgLeuGlnSerGlyVal 382

Db 112 ---CCCGGT-----GACTTAGCTCGCTCTCCAGTAAGTACTCCAGGCTTC 156
Qy 383 AsnThrLeuGlnGlyPheLysGluAspLysArgAsnLysValThrProValLeuTyrcys 402
Db 157 ACCAGCGCTG---GACTTCAAGACGAGAGAAAGAAAGAACTACCC-----TTCTC 204
Qy 403 AsnTyrcylProTyrcSerSerTyrcAlaProHisTyrcAspSerThrPheAlaAsnIleSer 422
Db 205 TCC---AGTGCACACTACTGCGCTTTGATGCAGAAATATATTCAGATTTGGCGACTTGA 261
Qy 423 LysAspAspSerAspLeuIleTyrcSerThrTyrcGlyGluAspSerAspLeuProSerAsp 442
Db 262 TCCGACGAGATGAGTGGCTCTACTACAGCTTACGAGATAGACAGCGCTGAGTGGC 321
Qy 443 PheSerIleHisGluPheLeuAlaThrCysGlnAspTyrcProTyrcValMetAlaAspSer 462
Db 322 CTGAGCCTGCAAGAGTGTGAGAGATGCTGGAGCTACAGCAAGAAAGTGTGAGAC 381
Qy 463 LeuLeuAspValLeuThrysglygllyhiseraThrleuGlnGluMecglu----- 480
Db 382 CTCTGAGCCAGATTCACAGCGGAGACCACTTACAGACGCTCTTCCAGCTGAAGCAGAGA 441
Qy 481 -----MetSerleuprogluaspGluylhisThrArgThrleu---AspThr 495
Db 442 AGAAATGTTCCATGAAGCTCCAGATGAAGCAAGTTGGGAGACCCCTAGAGACAGC 501
Qy 496 GlyLysGluMecgluGlnIleThrgluValGluProProgllyArgleuaspSerThr 515
Db 502 AGCAGCTGTGTTGAGATTCATGTCATGAAG-----TCTTAT 540
Qy 516 GlnAspArgleuIleAlaLeuLysAlaValThrAspPheglYValProValGluValPhe 535
Db 541 CCGGAGCTTCTGTGATATCTCATGCTCTCTGGGAAAGTGAAGAGAGAGCTG 600
Qy 536 AspSerGluLysAlaGluIlePheGlnLysLysLeuaspGluThrThrArgleuLysArg 555
Db 601 GACCTGACAGACGACCATTTG-----AACTGGATGAGACGAGAAAGCTCTGACAG 651
Qy 556 GluLeuGlnGlnAlaGlnAsnGluArgLeuSerThrArgProProgllyAsnMetIleCys 575
Db 652 GACCTCAGACGAAACAGAGGCGGAGGCTCTGCGCTCTGCTCAACCTCAGCTCC 710
Qy 576 LeuLeuGlyProSer 580
Db 711 CTGTCCAGCGCTTC 725

RESULT 14
US-09-864-761-11927
; Sequence 11927, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667

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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 11927
; LENGTH: 577
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC016498.4
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
; US-09-684-761-11927

Alignment Scores:
Pred. No.: 1,2e-12 Length: 577
Score: 215.50 Matches: 44
Percent Similarity: 78.31% Conservative: 21
Best Local Similarity: 53.01% Mismatches: 9
Query Match: 7.01% Indels: 9
DB: 9 Gaps: 3

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QY 10 SerAspLyshIseuTyrgIuGluTyVaIGluLySProlEuLySleuValleuLyVal 29
DB 98 GCCGCAAGCCCTG-----GAGAAAGCCTTAAGCTAGTCTGGAAGGTC 142
QY 30 GlyGIyAsnGIuValThrgIuLeuSerThrgIySerGIyhiAspSerLeuPhe 49
DB 143 GGAGGAAGTGAAGTGAAGTGAAGTCA-----GGATCCGGCCAGCACTCCAGTTACTAT 196
QY 50 GluAspLyshIseuTyrgIuGluTyVaIGluLySProlEuLySleuValleuLyVal 67
DB 197 GATGCAAGTGAAGTGAAGTGAAGTGAAGTCA-----GGATCCGGCCAGCACTCCAGTTACTAT 256
QY 68 LysGIyGIuLyGIuValThrgIuLeuSerThrgIySerGIyhiAspSerLeuPhe 87
DB 257 AAGTCCGAAAGGAAGCAATCTGACATGAGAAAGGAAGCAAGCAAGTAAAGGAG 316
QY 88 AspLyshIseuTyrgIuGluTyVaIGluLySProlEuLySleuValleuLyVal 90
DB 317 CAGCGGCGG 325

RESULT 15
US-09-764-887-619
; Sequence 619, Application US/09764887
; Patent No. US20020042096A1
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; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA113
; CURRENT APPLICATION NUMBER: US/09/764,887
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 658
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 619
; LENGTH: 32222
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-764-887-619

Alignment Scores:
Pred. No.: 3.35e-10 Length: 32222
Score: 215.50 Matches: 44
Percent Similarity: 78.31% Conservative: 21
Best Local Similarity: 53.01% Mismatches: 9
Query Match: 7.01% Indels: 9
DB: 9 Gaps: 3

US-09-687-230A-2 (1-589) x US-09-764-887-619 (1-32222)
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DB 25013 GCCGCAAGCCCTG-----GAGAAAGCCTTAAGCTAGTCTGGAAGGTC 25057
QY 30 GlyGIyAsnGIuValThrgIuLeuSerThrgIySerGIyhiAspSerLeuPhe 49
DB 25058 GAGGAAGTGAAGTGAAGTGAAGTCA-----GGATCCGGCCAGCACTCCAGTTACTAT 25111
QY 50 GluAspLyshIseuTyrgIuGluTyVaIGluLySProlEuLySleuValleuLyVal 67
DB 25112 GATGCAAGTGAAGTGAAGTGAAGTGAAGTCA-----GGATCCGGCCAGCACTCCAGTTACTAT 25171
QY 68 LysGIyGIuLyGIuValThrgIuLeuSerThrgIySerGIyhiAspSerLeuPhe 87
DB 25172 AAGTCCGAAAGGAAGCAATCTGACATGAGAAAGGAAGCAAGCAAGTAAAGGAG 25231
QY 88 AspLyshIseuTyrgIuGluTyVaIGluLySProlEuLySleuValleuLyVal 90
DB 25232 CAGCGGCGG 25240

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Job time : 515 secs
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 27, 2003, 01:05:34 ; Search time 107 Seconds
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Title: US-09-687-230A-2
Perfect score: 3073
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdt
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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5: /cgn2_6/ptodata/2/ina/PTCUS.COMB.seq: *
6: /cgn2_6/ptodata/2/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3073	100.0	2307	3	US-08-942-008-1
2	745	24.2	477	4	US-08-747-562-29
3	258.5	8.4	4549	4	US-09-620-312D-266
4	258.5	8.4	4942	4	US-09-620-312D-267
5	227	7.4	8147	4	US-09-514-247A-9
6	205	6.7	7326	4	US-08-194-468-1
7	205	6.7	7326	4	US-08-514-247A-7
8	205	6.7	7344	3	US-08-961-739-1
9	198	6.4	2330	2	US-08-557-128-3
10	198	6.4	2330	2	US-09-242-690A-34
11	192.5	6.3	5477	4	US-09-535-008-74
12	191	6.2	5480	4	US-09-535-008-70

13	191	6.2	5564	4	US-09-535-008-68	Sequence 68, Appl
14	190.5	6.2	9046	1	US-08-227-536-1	Sequence 1, Appl
15	190.5	6.2	9046	5	PCT-US95-04682-1	Sequence 1, Appl
16	189.5	6.2	5567	4	US-09-535-008-64	Sequence 64, Appl
17	188.5	6.1	5468	4	US-09-535-008-66	Sequence 66, Appl
18	188.5	6.1	5573	4	US-09-535-008-76	Sequence 76, Appl
19	187	6.1	5386	4	US-09-535-008-60	Sequence 60, Appl
20	187	6.1	5471	4	US-09-535-008-1	Sequence 1, Appl
21	187	6.1	5471	4	US-09-535-008-62	Sequence 62, Appl
22	187	6.1	5576	4	US-09-535-008-72	Sequence 72, Appl
23	181.5	5.9	5962	1	US-08-188-582-10	Sequence 10, Appl
24	181.5	5.9	5962	1	US-08-646-715-10	Sequence 10, Appl
25	170.5	5.5	4164	1	US-08-188-582-3	Sequence 3, Appl
26	170.5	5.5	4164	1	US-08-646-715-3	Sequence 3, Appl
27	159	5.2	6755	3	US-08-931-999-4	Sequence 4, Appl
28	154	5.0	8789	1	US-08-328-254-5	Sequence 5, Appl
29	153	5.0	3104	4	US-09-418-780A-2	Sequence 2, Appl
30	151	4.9	4868	4	US-08-139-937-12	Sequence 12, Appl
31	151	4.9	4868	5	PCT-US93-11310-12	Sequence 10, Appl
32	150.5	4.9	5893	2	US-08-687-080-44	Sequence 44, Appl
33	150	4.9	5893	4	US-08-938-105-2	Sequence 2, Appl
34	149.5	4.9	5893	1	US-08-592-126-54	Sequence 54, Appl
35	149.5	4.9	5893	4	US-09-168-595-54	Sequence 54, Appl
36	147.5	4.8	4766	5	PCT-US93-07261-10	Sequence 10, Appl
37	147	4.8	9551	1	US-08-056-200-93	Sequence 93, Appl
38	147	4.8	9551	2	US-08-800-644-93	Sequence 93, Appl
39	146.5	4.8	4892	4	US-09-620-312D-1065	Sequence 1065, Ap
40	145.5	4.7	8257	4	US-09-595-684B-30	Sequence 30, Appl
41	145.5	4.7	8503	4	US-09-620-312D-130	Sequence 10, Appl
42	144	4.7	2527	4	US-09-555-790A-1	Sequence 1, Appl
43	142	4.6	6773	4	US-09-166-350-27	Sequence 27, Appl
44	142	4.6	10136	1	US-08-353-700-2	Sequence 2, Appl
45	142	4.6	10136	5	PCT-US95-16216-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-942-008-1
Sequence 1, Application US/08942008
Patent No. 6133419
GENERAL INFORMATION:
APPLICANT: Braeilmann, Sylvia
TITLE OF INVENTION: Nucleotide Sequences that Encode
Phosphatidylinositol-3' Kinase Associated Proteins and
TITLE OF INVENTION: Uses Thereof
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: ONYX Pharmaceuticals, Inc.
STREET: 3031 Research Drive
CITY: Richmond
STATE: CA
COUNTRY: USA
ZIP: 94806
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/942,008
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Giotta, Gregory
REGISTRATION NUMBER: 32,028
REFERENCE/DOCKET NUMBER: ONYX1027
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 262-8710
TELEFAX: (510) 222-9758
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2307 base pairs

APPLICANT: WALLACH, David
APPLICANT: BOLDIN, Mark
APPLICANT: METT, Igor
APPLICANT: VAROLOMEV, Eugene
TITLE OF INVENTION: MODULATOR OF TNF/NGF SUPERFAMILY RECEPTORS
TITLE OF INVENTION: AND SOLUBLE OLIGOMERIC TNF/NGF SUPERFAMILY RECEPTORS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROMDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
City: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,562
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05854
FILING DATE: 11-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 109,632
FILING DATE: 11-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 111,125
FILING DATE: 02-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROMDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH-15A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 477 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..477
US-08-747-562-29
Alignment Scores:
Pred. No.: 2,46e-73 Length: 477
Score: 745.00 Matches: 153
Percent Similarity: 95.62% Conservative: 0
Best Local Similarity: 95.62% Mismatches: 2
Query Match: 24.24% Indels: 5
DB: 4 Gaps: 0
US-09-687-230a-2 (1-589) x US-08-747-562-29 (1-477)
QY 270 GlyCysTrpGlnArgGluArgGluAspSerGlyAspAlaGluAlaHisAlaPheLeuSse 289
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QY 289 rProSerLysGluAsnLysLysLysAspLysAspMetLeuGluAspLysPheLysSerAs 309
Db 63 TCCACAGAAAGAAATATATAAAGAAAGCAAGATATCTGAAAGATTAAGTTTAAAGCAA 122
QY 309 naenLeuGluArgGluGlnGluGlnLeuAspArgIleValLysGlnSerGlyGlyLysLe 329
Db 123 TAAATTAGAGAGAGAGAGAGAGAGAGCTTGACCCGATCGTAAAGAAATCTGAGAGAAAGCT 182
QY 329 uThrArgLysLeuValAsnSerGlnCysGluPheGluArgGlyAspProAspGlyThrTh 349

Db 183 GACCAGCGGCTTGTAACAGTCAGTCGGAATTTGAAGAAAGAAACCAAGTAGAACAC 242
QY 349 rThrLeuGlyLeuLeuHisProValAspProIleValGlyGluProGlyTyrCysLeuVa 369
Db 243 GACCTGGAGCTTCTCCATCTCTGATCCATGATCCATGATGAGACACAGGCTACTGCTGT 302
QY 369 lArgLeuGlyMetThrThrGlyArgLeuGlnSerGlyValAsnThrLeuGlnGlyPheL 389
Db 303 GAGACTGGGAAATACAACTGAGAGAGACTTCACTGCTGAGGTGAATTAATTTCAGGGGTTCA 362
QY 389 sGluAspLysArgAsnLysValThrProValLeuTyrLeu-AsnTyr-GlyProTyrSer 408
Db 363 AGAGATTAAGAAAGAAAGCAAGTCACTCAGTGTATATTGGAATTAATGAGGCCCCCTACAGT 422
QY 409 Ser-TyrAlaProHisTyrAspSerThrPheAlaAsn-IleSerLysAsp 424
Db 423 TCTTATGACCGCATTAATGATCTCCACATTTCGAAATTAATACAGAGAGAT 472
RESULT 3
US-09-620-312D-266
Sequence 266, Application US/09620312D
GENERAL INFORMATION:
PATENT No. 6569662
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aiding J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yundong
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662e1 Nucleic Acids and
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: PC_FL_genes Version 1.0
SEQ ID NO 266
LENGTH: 4549
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (186) ..(3362)
US-09-620-312D-266
Alignment Scores:
Pred. No.: 6,15e-18 Length: 4549
Score: 256.50 Matches: 109
Percent Similarity: 36.85% Conservative: 62
Best Local Similarity: 23.49% Mismatches: 136
Query Match: 8.41% Indels: 157
DB: 4 Gaps: 15
US-09-687-230a-2 (1-589) x US-09-620-312D-266 (1-4549)
QY 11 AspLysHisLeuTyrGlnGluTyrValGluLysProLeuLysLeuValLeuLysValGly 30
Db 1341 GATGTCACACCGCTCCAGGCTGCACCGAGGCTCTGAATATTACGGGAGATGTC--- 1397

```

Qy 31 GlyanGluValThrGluLeuSer-ThrGlySerSerGlyHisAspSerSerLeuPheGlu 50
Db 1398 -----GAAATCAAAAATGGCTCTGTGCAAAAAGAGAGCTCGATTAAAAAG 1442
Qy 51 AspyAsnAsnAsnHisAspLysHisLeuAspArgLysLysArgLysLysGlu 70
Db 1443 GTCAAGTCC-----ACATCCAAAGTCAGAGAAAGGCAAAAAGAGCTTAAG 1487
Qy 71 Lys-----GlnHisProGly 75
Db 1488 AAGACTGTGCTGAGCCCTGCGCGCTCTGCGACCGTGTGCTCTTATATTCCTCCCG 1547
Qy 76 GluGluLysGluArgLysArgArgValLysGluAspLysLysLys----- 91
Db 1548 CAGAGCTTAATAGGATTGGCAATCAGGTGGCCATTACGCGAAAGAACAGTTGTGGAG 1607
Qy 91 ----- 91
Db 1608 CGAGCCCAAGCTACTGCTGCTCAAGCGGCTGTCCAGGAAGGGGCCCCCTGCTGCG 1667
Qy 92 -----ArgAspArgAspArgVal 97
Db 1668 CGGCTGAGTCCAGCTGCACTGCTCAGCGAACTCACAGCAGAGAAATGATGAGAGAG 1727
Qy 98 GluAsnGluValGluLysAspLeuGlnCysHisAlaProValArgLeuAspLeuPro 117
Db 1728 ATGAAGCTGCCCAAGAGAGAGCTGAAGTACGACCGGCTGCGCAGACCTGAGAGCGC 1787
Qy 118 GluLysProLeuThrSerSerLeuAlaLysGlnGlu-----Glu 130
Db 1788 GCTGCGCTGCTGATCGAGCTCTGCGCAAGCGGAGAAAGCTCAAGCTGAGCAGGTGAG 1847
Qy 131 ValGluGln-----ThrProLeuGlnGluAlaLeuAsnGlnLeu 143
Db 1848 GTGAGCAGGCTCGCCATGAGAGCTGCGCTGACCCGCTGAGCGGTGCTGCTGCTCATG 1907
Qy 144 MetArgGlnLeuGlnArgLysAspProSerAlaPhePheSerPheProValThrAsp 163
Db 1908 CTGACCGCTGCTCAAGACAGAGAGAGAGAGAGAGAGATTTGGCGAGCCGCTGATGAG 1967
Qy 164 IleAlaProGlyTyrSerMetIleLeuHisAspPheAspPheSerThrMetLysGlu 183
Db 1968 GAGGACCAAGATTTATTTGATCACTTAACTTCCATCGAGCTTGGCACAATGAGGAA 2027
Qy 184 LysIleLysAsnAsnAspTyrGlnSerIleGluGluLeuLysAspAsnPheLysLeu 203
Db 2028 CGGTTAGAAAGCTCAAGCGTATTAACCTTCATGAGTTTGAGAGAGATTTGATCTCAT 2087
Qy 204 CysThrAsnAlaMetIleTyrAsnLysProGluThrIleTyrTyrAlaAlaLysLys 223
Db 2088 ATGATATTACTCAAGTAAATGACATGACCGAGACCGGTGTTATGAGCGCGGTGAG 2147
Qy 224 LeuLeuHisSerGlyMetLysIleLeuSerGlnGluValGlnSerLeuLysGlnSer 243
Db 2148 CTGCGCCATCAAGGAGGCTGTTCTGTGAGCAGCGCCG----- 2186
Qy 244 IleAspPheMetAlaAspLeuGlnLysThrArgLysGlnLysAspGlyThrAspThr 263
Db 2186 ----- 2186
Qy 264 GlnSerGlyGluAspGlyGlyCysThrProLysArgGluAspSerGlyAspAlaGlu 283
Db 2187 -----CGCGAGGTGACAGCAGCATCGGCTTGAGAAAG 2216
Qy 284 Ala-----HisAlaPheLysSerProSerLysGluAsnLysLys----- 296
Db 2217 GCTTCGGGAGTCACTCTGAGAGGCTCTGCTGCGGAGACCGCGGCGCTTCTCTCG 2276
Qy 297 LysAspLysAspMetLeuGluAspLysAspLysSerAsnAsnLeu-----GluArg 313
Db 2277 GAAAGCTGTGACAGGTTGCTGTGAGACCCGCCCAACAGAGCCCACTGCGGCTGAGAGAG 2336

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Qy 314 GluGlnGluLeuAspArgIle-----ValLysGlnSerGlyLys 328
Db 2337 CTGAGAGAGCTGTGAGCAGTCTGACCTCAGCTGCGCTGATGAGTCAAGCGGCTCCCG 2396
Qy 329 LeuThrArg---ArgLeuValAsnSerGlnCysGluPheGluArgLysProAspGly 347
Db 2397 AGCAAGCGGCAAGCTGCTCAAAAAGAAATTCCTTCTCCGAAACAG----- 2447
Qy 348 ThrThrThrLeuGlyLeuLeuHisProValAspProIleValGlyLysProGlyTyrCys 367
Db 2448 -----CTGAGCCAGCAGCAGCAGC---CAGCCCTGCCAGCGGCGCAGC----- 2489
Qy 368 LeuValArgLeuGlyMetThrThrGluArgLeuGlnSerGlyValAsnThrLeuGlnGly 387
Db 2490 -----TTGGAAGGC 2498
Qy 388 PheLysGluAsp 391
Db 2499 TTCGAAAGAGAC 2510

```

RESULT 4

US-09-620-312D-267
 : Sequence 267, Application US/09620312D
 : Patent No. 6569662

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom
 APPLICANT: Liu, Chenghua
 APPLICANT: Xuendi, Yindod
 APPLICANT: Zhang, Jie
 APPLICANT: Ren, Feiyan
 APPLICANT: Chen, Rui-hong
 APPLICANT: Zhao, Qing A.
 APPLICANT: Wehrman, Tom
 APPLICANT: Xue, Aidong J.
 APPLICANT: Yang, Yonghong
 APPLICANT: Wang, Jiao-Rui
 APPLICANT: Zhou, Ping
 APPLICANT: Ma, Yundong
 APPLICANT: Wang, Dunhui
 APPLICANT: Wang, Zhiwei
 APPLICANT: John Tillinghast
 APPLICANT: Drmanac, Radje T.
 TITLE OF INVENTION: No. 6569662e1 Nucleic Acids and
 TITLE OF INVENTION: Polypeptides
 FILE REFERENCE: 784CIP28

CURRENT APPLICATION NUMBER: US/09/620,312D
 CURRENT FILING DATE: 2000-07-19
 PRIOR APPLICATION NUMBER: 09/552,317
 PRIOR FILING DATE: 2000-04-25
 PRIOR APPLICATION NUMBER: 09/488,725
 PRIOR FILING DATE: 2000-01-21
 NUMBER OF SEQ ID NOS: 1105
 SOFTWARE: pc_fl_genes Version 1.0
 SEQ ID NO 267
 LENGTH: 4942

TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (186)..(3755)
 US-09-620-312D-267

Alignment Scores:

Pred. No.: 7.03e-18 Length: 4942
 Score: 258.50 Matches: 109
 Percent Similarity: 36.85% Conservative: 62
 Best Local Similarity: 23.49% Mismatches: 136
 Query Match: 8.41% Indels: 157
 DB: 4 Gaps: 15

US-09-687-230A-2 (1-589) x US-09-620-312D-267 (1-4942)

Qy 11 AspyHisLeuTyrGluGluTyrValGluLysProLeuLysLeuValLeuLysValGly 30

Db 1341 GATGTCCACACGCTCCAGGCTGCACCCGAGGCTCGAATATTACGGGATGTC--- 1397
Qy 31 G1yAsnGluValThrGluLeuSerThrGlySerSerGlyHisAspSerLeuPheGlu 50
Db 1398 -----GAAATGAAATAATGGCTGTCTGAAAAGAGCTCGTTTAAACG 1442
Qy 51 AspLeuAsnAspHisAspLeuYH:leuAspArgLeuValGlyValGlyValGlyGlu 70
Db 1443 GTCAGGTC-----ACATCCAGGTCAGAGAGAGAGAGAGAGAGAGAGAGAG 1487
Qy 71 Lys-----GlnLeuProGly 75
Db 1488 AAGAGCTGTGAGCTGAGCCCTGGCGCTGTCGACCGGCTGCTTATATCCCGG 1547
Qy 76 G1G1uLysLeuValGlyValGlyValGlyValGlyValGlyValGlyValGlyVal 91
Db 1548 CAGAGGTTAAATAGATTGGAAATCAGTGGCCATTGACGGAGAGAGAGAGAGAG 1607
Qy 91 ----- 91
Db 1608 CAGAGCCACAGCTACTGCTGCTCAGACGCTGTCCAGAGAGAGAGAGAGAGAG 1667
Qy 92 -----ArgAspArgAspArgVal 97
Db 1668 CGGCTGAGTCCAGCTGCACTGTCAGAGAGAGTCAAGAGAGAGAGAGAGAGAGAG 1727
Qy 98 G1uAsnGluValGlyValGlyValGlyValGlyValGlyValGlyValGlyValGly 117
Db 1728 ATGAGAGCTCCAAAG 1787
Qy 118 G1uLysProLeuThrSerSerLeuValAlaLeuGlu-----Glu 130
Db 1788 GCTCGCTGCTGATCGAGCTGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1847
Qy 131 ValGluGln-----ThrProLeuGlnGluAlaLeuAsnGlu 143
Db 1848 GTGAGAGAGAGTCCGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1907
Qy 144 MetArgGlnLeuGlnValGlyValGlyValGlyValGlyValGlyValGlyValGly 163
Db 1908 CTGACAGCTGCAAG 1967
Qy 164 IleAlaProGlyThrSerMetIleIleLeuHisProMetAspPheSerThrMetLeuGlu 183
Db 1968 GAGGTACCAATTTATTTGATTCACATTAAATCCCATGAGCTTGGCCAAATGAGGAA 2027
Qy 184 LysIleLeuAsnAsnAspArgGlnSerIleGluLeuLeuValAspAsnPheLeuMet 203
Db 2028 CGGTTAGAACTCAAGGCTATAAAACCTCATGAGAGTTTGAAGAGATTTGATTCATT 2087
Qy 204 CysThrAsnAlaMetIleTyraAsnLysProGluThrIleTyryTyryAlaAlaLysLys 223
Db 2088 ATGATTAACATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 2147
Qy 224 LeuLeuHisSerGlyMetLysIleLeuSerGlnGluArgIleGlnSerLeuValGlnSer 243
Db 2148 CTGCGGATCAGAGAGAGTGTGTTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2186
Qy 244 IleAspPheMetAlaAspLeuGlnLysThrArgLysGlnLysAspGlyThrAspThrSer 263
Db 2186 ----- 2186
Qy 264 GlnSerGlyGluAspGlyGlyCysTrpGlnArgGluArgGluAspSerGlyAspAlaGlu 283
Db 2187 -----CGCGAGGTGAGACAGATCGGCTTGAAGAG 2216
Qy 284 Ala-----HisAlaPheLysSerProSerLysLeuLysLysLys 236
Db 2217 GGCCTCGGAGATGACCTGCTGAGCGGCTGCTGCGGACCGCGGCTTCTCTCTGG 2276
Qy 297 LysAspLysAspMetLeuGluAspLysPheLysSerAsnLeu-----GluArg 313
Db ----- 313

Db 2277 GAAGACGTGACAGAGTTGCTGACCCCGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 2316
Qy 314 G1uGlnGlnLeuPheArgIle-----ValLysGlnSerGlyLys 328
Db 2337 CTGAGAGAGCTGCTGAGATGCTGACCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTG 2396
Qy 329 LeuThrArg-----ArgLeuValAsnSerGlnPheGluArgArgArgProAspGly 347
Db 2397 AGCAGCGGAGAGAGCTGCTCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2447
Qy 348 ThrThrThrLeuGlyLeuLeuHisProValAspProIleValGlyGluProGlyTyrcys 367
Db 2448 -----CTGAG 2489
Qy 368 LeuValArgLeuLysMetThrThrThrArgLeuGlnSerGlyValAlaThrLeuGlnGly 387
Db 2490 -----TTGAGAGAG 2498
Qy 388 PheLysGluAsp 391
Db 2499 TTGAGAGAGAGAG 2510

RESULT 5
US-09-514-247A-9
Sequence 9, Application US/09514247A
Patent No. 6365361
GENERAL INFORMATION:
APPLICANT: TANABE SEIYAKU CO. LTD.
APPLICANT: TANIGUCHI, Tomoyasu
APPLICANT: MIZUKAMI, Junko
TITLE OF INVENTION: METHOD FOR IDENTIFYING OR SCREENING AGONIST AND ANTAGONIST TO PPA
FILE REFERENCE: TANIGUCHI-6
CURRENT APPLICATION NUMBER: US/09/514, 247A
CURRENT FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: PCT/JP98/03734
PRIOR FILING DATE: 1998-08-24
PRIOR APPLICATION NUMBER: JP231084/1997
PRIOR FILING DATE: 1997-08-27
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.0
SEQ ID NO 9
LENGTH: 8147
TYPE: DNA
ORGANISM: human
FEATURES:
NAME/KEY: CDS
LOCATION: (819)..(8147)
US-09-514-247A-9

Alignment Scores:
Pred. No.: 4.8e-14 Length: 8147
Score: 227.00 Matches: 149
Percent Similarity: 34.18% Conservative: 80
Best Local Similarity: 22.24% Mismatches: 214
Query Match: 7.39% Indels: 227
DB: 4 Gaps: 30

US-09-687-230A-2 (1-589) x US-09-514-247A-9 (1-8147)
Qy 36 G1uLeuSerThrGlySerSerGlyHisAspSerSerLeuPheGluAspLysAsnAsp--- 54
Db 3762 GAACCAATTCACAG 3821
Qy 55 -----HisAspLysHisLysAspArgLysArgLysArgLysArgLysArgLysGln 72
Db 3822 CAGCAG 3845
Qy 73 IleProG1G1uGlyValGlyValGlyValGlyValGlyValGlyValGlyValGlyVal 88
Db 3846 -----CTGCTGATCCAAAG 3902
Qy 89 -----LysLysLysArgAspArgArgValG1uAsnG1uLysG1uLysAspLeuGln 106
Db ----- 106

Db 3903 GCTTCCCAAGTTAAAGAAACAGACATAGCAGAGAAATCAGAA----- 3950
 Qy 107 CyehialapProvalaGleuAapleuProProGluYleuProleuThrSerSerleuAla 126
 Db 3951 -----CCAAATGGAAGTGGAT-----GAAAGAAACCTGAAAGTGAAGAGATT 3995
 Qy 127 LysGlnGlnGlnValGlnGlnThr----- 134
 Db 3996 AAGAGAGAAAGAGAGTAGCAGTAACGCGACAGCCTCTCAGTCAACATCTCTCCAG 4055
 Qy 135 -----ProleuGlnGlnValaleuAanglnLeuMetArg 145
 Db 4056 CCGCGCAAAAATCTTTAAACAGAGAGAGTACGCGAGCCCTCATGCCAACCTCGAA 4115
 Qy 146 GlnleuGlnArgYsaapProSerAlaPhe---PheSerPheProValThrAspPheIle 164
 Db 4116 GCATCTGATGACGACGAGCCAGAGCTTACCTTCCGCGAGCCTGTAGATCCCACTC 4175
 Qy 165 -----AlaProGluYrSerMetIleIleYshIsprometAspPheSerThrMetIys 182
 Db 4176 CTGCGAATTCAGACTTTTGTGACATGTGAAGATCCCATGACCTCTCCACCATCAG 4235
 Qy 183 GlnYsaIleYsaAenAspYrGlnSerIleGlnleuYsaAspAsnPhelYleu 202
 Db 4236 CCGAAGCTGGACACAGGCAATACCAAGAGCCCTGCGAGTACGACAGAGCTGGCTC 4295
 Qy 203 MetCysThrAsnAlaMetIleYrAsnYsaProGluThrIleYrYrYsaAlaAlaYls 222
 Db 4296 ATGTTCACACATGCTGCTCTATATCGCAAGACATCCGAGCTCTAAATTTTGAGT 4355
 Qy 223 LysleuLeuThrseryGlnMetIleYsaIleuSerGlnGlnArgIleGlnSerIleGln 242
 Db 4356 AAGCTT-----GCAGAGCTTTAGAGAGAA---ATTGACCTGTATGATGAG 4400
 Qy 243 SerIleAspPheMetAla----- 248
 Db 4401 TCCCTTGATATTCCTGTGACGACGATGATGATTTCCCAAGACTTTGTGCTGAT 4460
 Qy 249 AspleuGlnYsaIleYsaGlnYsaIleYsaIleYsaIleYsaIleYsaIleYsa 268
 Db 4461 GCGAAGACGCTGTACCATTCCTCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCT 4520
 Qy 269 GlnYsaIleYsaIleYsaIleYsaIleYsaIleYsaIleYsaIleYsaIleYsa 282
 Db 4521 CATTTCTGTGAAGTGTTCACAGAGATCCAGGCGAAGATGACCTCGGAGTAC--- 4577
 Qy 283 GlnAlaIleYsaIleYsaIleYsaIleYsaIleYsaIleYsaIleYsaIleYsa 302
 Db 4578 -----GACCTTTCACAGCCCAAGACGACAAATTTCAAGATCAGTTT 4619
 Qy 303 GlnAspYsaIleYsaIleYsaIleYsaIleYsaIleYsaIleYsaIleYsaIle 312
 Db 4620 GAAAGAGAG---AAAAATGATACCTTAGACCCCAACCTTTCGTTGATTCAGAGAGTGT 4676
 Qy 313 ---ArgGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 318
 Db 4677 GCGCGAAGATGATCAGATTTGCGCTTCTGCAATATGATCATTTGCGCTTCAAGTTT 4736
 Qy 319 ---AspArgIleValYsaIleYsaIleYsaIleYsaIleYsaIleYsaIleYsa 326
 Db 4737 GTGTCGACAACTCTGTAAGAAACCTGCGAGACTGCGAAGAAACAAATTCAGTGTCT 4796
 Qy 327 -----GlnYsaIleYsaIleYsaIleYsaIleYsaIleYsaIleYsaIleYsa 341
 Db 4797 AAGAGCTGACAGACACACAGAGCTGGAACCACTTGGAAGCCGAGTGAAACAAATTTTGTG 4856
 Qy 342 ArgArgYsaIleYsaIleYsaIleYsaIleYsaIleYsaIleYsaIleYsaIle 361
 Db 4857 CCGCGCCCAAGT-----CACCTT----- 4874
 Qy 362 GlnYsaIleYsaIleYsaIleYsaIleYsaIleYsaIleYsaIleYsaIleYsa 381
 Db 4875 ---GAAGCCGGGAGGTTTTTGTGCGAGTGTGCGCAGCTCA----- 4913

Qy 382 ValAsnThrleuGlnGlnYsaIleYsaIleYsaIleYsaIleYsaIleYsaIleYsa 400
 Db 4914 -----GACAAAGCGTGAAGTCAAGCCCGGATGAAG 4946
 Qy 401 ---TyrlleuAsnYrGluYrProYrSerSerYrAlaProHis---YrAspSerThr 417
 Db 4947 TCAAGTTGTGATCTGGGAAATGTGTGATCTTTCCATATCGAACCAAGACTCTG 5006
 Qy 418 PheAlaAsnIleSerYsaAspAspSerAspIleYr-----SerThr 432
 Db 5007 TTTGCTTTGAGGAAATTAAGCGCGTGAATGTCTGCTTTTGGATGACAGTCCAAAGAA 5066
 Qy 433 TyrGlnYsaIleYsaIleYsaIleYsaIleYsaIleYsaIleYsaIleYsaIle 444
 Db 5067 TACGCTCTGATTTCCCTCCCAACAGAGCGGTGTACATTTCTTATCTGATAGT 5126
 Qy 445 IleHisGlnPheleuAlaThrCys-GlnAspYrProYrValMetAlaAspSerleu 464
 Db 5127 ATTCAATTTCTCCGCGCAGCTGCTCCGACAGCGGTTTACATGAGA---TCTTATT 5183
 Qy 464 ValAspVal-----LeuThrYsaIleYsaIleYsaIleYsaIleYsaIleYsa 476
 Db 5184 GATATTATAGATGATGAAGAAATTAAGGTATGTGACAGGCAATCTGGGCTGTCT 5243
 Qy 476 GlnGlnMetGlnMetSerleuProGluAspGlnYsaIleYsaIleYsaIleYsa 489
 Db 5244 CCAAGTGAAGAGATGATTTATCTTCCATTCGACCCACTGATCAAAATATCCAG 5303
 Qy 490 -----ThrArgThrleuAspThrGln 497
 Db 5304 CCAAAAGCTGACGAGAGTGTACAAAGAGTGTGACAAAGCGTTTGACAGCGGATC 5363
 Qy 497 GlnMetGln-GlnIleThrGlnValGlnProProGlnYsaIleYsaIleYsaIle 516
 Db 5364 ATCCATGATCAACA-----GGATATTTCAACAGCAACTGAA 5402
 Qy 517 AspArgleuIleAlaIleYsaIleYsaIleYsaIleYsaIleYsaIleYsaIle 536
 Db 5403 GACAGCTTCCAGCTGCAAGAGAGTCCCTATTT----- 5438
 Qy 537 SerGlnGlnAlaGlnIlePheGlnYsaIleYsaIleYsaIleYsaIleYsaIleYsa 556
 Db 5439 ---GAAGTATTTCTGCGCAATGTGTGAAGAGAGC-----ATTAAGAA 5483
 Qy 557 LeuGlnGlnAlaGlnIleYsaIleYsaIleYsaIleYsaIleYsaIleYsaIle 564
 Db 5484 CTAGAACAGAGAGAGAGAGAGG 5507

RESULT 6
 US-08-194-468-1
 : Sequence 1, Application US/08194468
 : Patent No. 5750336
 : GENERAL INFORMATION:
 : APPLICANT: Montminy, Marc R.
 : TITLE OF INVENTION: ASSAYS FOR THE IDENTIFICATION OF
 : TITLE OF INVENTION: COMPOUNDS WHICH INHIBIT ACTIVATION OF CAMP AND MITOGEN
 : NUMBER OF SEQUENCES: 3
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
 : STREET: 444 South Flower Street, Suite 2000
 : CITY: Los Angeles
 : STATE: California
 : COUNTRY: USA
 : ZIP: 90071
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent in Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/194,468

```

1 CILING DATE: 10-FEB-1994
2 CLASSIFICATION: 435
3 ATTORNEY/AGENT INFORMATION:
4 NAME: Reiter, Stephen E.
5 REGISTRATION NUMBER: 31,192
6 REFERENCE/DOCKET NUMBER: P41 96722
7 TELECOMMUNICATION INFORMATION:
8 TELEPHONE: (619)-546-4737
9 TELEFAX: (619)-546-9392
10 INFORMATION FOR SEQ ID NO: 1:
11 SEQUENCE CHARACTERISTICS:
12 LENGTH: 7326 base pairs
13 TYPE: nucleic acid
14 STRANDEDNESS: single
15 TOPOLOGY: linear
16 MOLECULE TYPE: DNA (genomic)
17 HYPOTHEetical: NO
18 ANTI-SENSE: NO
19 FEATURE:
20 NAME/KEY: CDS
21 LOCATION: 1..7323
22 US-08-194-468-1

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Db      3967 AACAAATTCAGTCTAAGAGCTGACAGACCAACAGATTGGAAACCACTTAGAAGACAGA 4026
Qy      337 GlnCysGluPheGluGlyArgGlyProArgProGlyThrThrThrLeuGlyLeuLeuHisPro 356
Db      4027 GTGAATAGATTGTTGGCGCGCAGAAAT-----CACCTT 4059
Qy      357 ValAspProIleValGlyGluProGlyTyrCysLeuValArgLeu----- 371
Db      4060 -----GAAAGCTGGGAGGTTTGTCCAGAGTGGGCGCAGCTCAGAC 4101
Qy      372 -----GlyMetThrThrGlyArgLeuGlnSerGly----- 381
Db      4102 AAGACTGTGAGGTCAAGCCGGAATGAAGTGGTTGTGATCTCGAGAGATGTGCG 4161
Qy      382 -----ValAspThrLeuGlnGlyPheLeuGly----- 390
Db      4162 GAATCTTTCCCATATGCTACCAAGACACTCTTGTGCTTTGAGAGATGATGAGTGCAT 4221
Qy      391 -----AspLysArgAsnLysValThr 397
Db      4222 GTGTGCTTTTGGATGATGTCAGAAATACGCTGTGATGCCCCCAAAATACAA 4281
Qy      398 ProValLeuTyrLeuAsnTyr-GlyProTyrSerSerTyrAla----- 411
Db      4282 GGGCTGTATACATATCTTATCTGGAACAGTATTCATTCTCCGGCCCGCTGCTCCGG 4341
Qy      412 -----ProHis-----T 414
Db      4342 AACAGCTGTTTACCATGAGATCTCATGATCTCGATATCTGAAATATGCTGAT 4401
Qy      414 YAspSerThrPheAlaAsnIleSer---Lys-AspAspSerAspLeuIleTyrSerThr 432
Db      4402 GTACACGACATATTTGGCGCTGTCCCAAGTGAAGAGATGACTATATCTTTCATTGC 4461
Qy      433 TyrGlyGlyAspSerAspLeuProSerAspPheSerIleHisGluPheLeuAlaThrCys 452
Db      4462 CACCCCGCTGACCAAGAAATCCCAACCAAGAAAGACTACAGAGTGTCAAGAAAGATG 4521
Qy      453 GlnAspTyrProTyrVal-----MetAlaAspSerLeuLeuAspValLeuThrLysGly 470
Db      4522 CTCGACAGGCGCTTGGACAGAGATCATTAACGACTATTAAGACATCTTCAAAACAGCG 4581
Qy      471 GlyHisSerArgThrIleuGlnGluMetSerLeuProGluAspGluGlyHisThr 480
Db      4582 AACGAAGACAGGCTCAGAGTCCCAAGAGTGCCTTATTTGAAGAGATTTCTGGCCT 4641
Qy      491 ArgThrLeuAspThrGly---LysGluMetGluGlnIleThrGluValGluProGly 509
Db      4642 AATGTGTGGAAGAAAGCACTTAAGAACTAGAACAA-----GAAGAAAGAAAGAAAGAA 4695
Qy      510 ArgLeuAspSerSerThrGlnAsp-ArgLeuIleAlaLeuLysAlaValThrAsnPheG 529
Db      4696 AAAGAGAGAGGTACTCAGAGAGTGCAGACTCTGAGGGCAGTCAAGGTGACA----- 4747
Qy      529 yValProValGluValPheAspSerGluGluIlePheGlnLysLeuAspG 549
Db      4748 -----GCAAAATGCGAAAGAAAGAA----- 4768
Qy      549 uThrThrArg-----LeuLeu-ArgGluLeuGlnGluAlaG 561
Db      4769 -ACAACAAGAAAGCAAAACAAACAAAGACATTTAGCCGCCCAACAAAGAAAGAGCC 4827
Qy      561 LAsnGlnLysArgLeuSerThrArgProProGlyLysAsnMetIleCys 575
Db      4828 AGCATGCCCAATGTTTCAACGACCTGTGCGAAGAGCTGATGC 4871

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RESULT 8
US-08-961-739-1
; Sequence 1, Application US/08961739A
; Patent No. 6063583
; GENERAL INFORMATION:
; APPLICANT: Montminy, Marc R.

```

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; TITLE OF INVENTION: Methods for Treating Diabetes Mellitus
; FILE REFERENCE: SALK1650-1
; CURRENT APPLICATION NUMBER: US/08/961,739A
; CURRENT FILING DATE: 1997-10-31
; EARLIER APPLICATION NUMBER: US 194,468
; EARLIER FILING DATE: 1994-02-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 7326
; TYPE: DNA
; ORGANISM: Mus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(7326)
; NAME/KEY: misc_feature
; LOCATION: (1)...(7326)
; OTHER INFORMATION: n = A,T,C or G
US-08-961-739-1

Alignment Scores:
Pred. No.      1,1e-11      Length:      7344
Score:         205.00      Matches:      150
Percent Similarity: 34.26%      Conservative: 96
Best Local Similarity: 20.89%      Mismatches: 237
Query Match:    6.67%      Indels:      235
DB:             3          Gaps:      30

US-09-687-230A-2 (1-589) x US-08-961-739-1 (1-7344)
Qy      32 AsnGluValThrGluLeuSerThrGlySerSerGlyHisAspSerSerLeuPheGluAsp 51
Db      2911 AATAGATCTCCCTAATCTCCCTGCTGACCAAGTCTGAAACCGATTCC-----CAGCAG 2964
Qy      52 LysAsnAspHisAspLysHisLysAspArgLysArgLysArgLysArgLysArgLys 71
Db      2965 CCAAGACCCGAGTGTGCCATGCTGGAATGAAGACAGAGTGCAGACATGATGCTGAG 3024
Qy      72 GlnIleProGlyGluGluLysGlyArgLysArgArgValGluLysGluAsp----- 88
Db      3025 CCTGAACCTAATGAAATCCAAAGGGGAACTCGGTGATGATGGAAGAGATTACAA 3084
Qy      89 -----LysLysLysArgAspArgAspArgValGluLysGlnLysGluLysAspLeu 105
Db      3085 GGTTCCTCCCAAGTAAAGAAAGACAGATACGACAGACAGACAGACAGACAGCA----- 3138
Qy      106 GlnCysHisAlaProValArgLeuAspLeuProGluLysArgProLeuThrSerSerLeu 125
Db      3139 -----ATGGAAGTAAAGAAAGAAAGAAACCTGAAGTAAAGTGCAGAA 3177
Qy      126 AlaLysGlnGluGluValGluGlnThr----- 134
Db      3178 GCTAAAGAGAAAGAAAGAGAAAGAGTTCGAACGACACAGCTCAATCAATCTCTCC 3237
Qy      135 -----ProLeuGlnGluAlaLeuAsnGlnLeuMet 144
Db      3238 CAGCCACGCAAAATAATCTTTAAACCCGAGAGCTACGCGCAGCACTTATGCCAACTTCA 3297
Qy      145 ArgGlnLeuGlnArgLysAspProSerAlaPhe---PheSerPheProValThrAspPhe 163
Db      3298 GAAGCACTTATTCGACAGACCCAGAGTCTTTGGCTTTTCGTGAGCTGTAGTCTCTCA 3357
Qy      164 Ile-----AlaProGlyTyrSerMetIleIleLysHisProMetAspPheSerThrMet 181
Db      3358 CTCCTAGAAATCCCAAGATTATTTGATATAGAAAGAAATCTATGAGACCTTCTTCAACATC 3417
Qy      182 LysGluLysIleLysAsnAsnAspTyrGlnSerIleGluGlnLysLeuLysAsnPheLys 201
Db      3418 AAACGAAGCTGACACAGCGCAATATCAAGAACCTGCGCAATGCTGATGATGTCAGG 3477
Qy      202 LeuMetCysThrAsnAlaMetIleTyrAsnLysProGluThrIleTyrTyrLysAlaAla 221
Db      3478 CTTATGTTCAACAAATGCGGTGCTATATATCGTAAAGCTCCCGTGTATTAATTTTGC 3537

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QY 222 LysLeuLeuLeuHisSerGlyMetLysIleLeuSerGlnGluArgIleGlnSerLeuLys 241
 DB 3538 AGTAACCTT-----GCAGAGCTTTTGAACAGAA---ATTGACCTGTCTGATG 3582
 QY 242 GlnSerIleAspMetAlaAspLeuGlnLysThrArgLysGlnLysAspGlyThrAsp 261
 DB 3583 CAGTCTCTTGATATTCCTGTGCA-----CGAAAGTATGAGTTCTCCCAAG 3630
 QY 262 Thr----- 262
 DB 3631 ACTTTGCTGTACGGAAGACAGCTGTGTACATTCCTGATGACGCTACTACAGC 3690
 QY 263 -----SerGlnSerGlyLysAspGlyLysTrp-----GlnArgGluArgGlu 277
 DB 3691 TATCAGATATGATATCTATTTCTGTGGAGGTTCACAGATCCAGGCGGAGAAATGTG 3750
 QY 278 AspSerGlyAspAlaGluAlaHisAlaPheLysSerProSerLysGluAsnLysLys 297
 DB 3751 ACCCTGGGTAC-----GACCTTCCCACTCAGACGACAAATT 3789
 QY 298 AspLysAspMetLeuGlnAspLysPheLysSerAsnAsnLeuLys----- 312
 DB 3790 TCCAAGATCAATTTGAAAGAG---AAAATGATACCTTAGTCTGAACCTTTGTT 3846
 QY 313 -----ArgGlnGlnGlnGlnLys----- 318
 DB 3847 GACTGCAAGAGTGTGCGGAGAGATGATCATGATTTGTCTTACATATGACATCAT 3906
 QY 319 -----AspArgIleValLysGlnSerGly----- 326
 DB 3907 TGGCCTTCAGGTTTGTGTGTGATCACTGTTGAGAAACTGACAGACCTCGGAAAGAA 3966
 QY 327 -----GlyLysLeuThrArgArgLeuValAsnSer 336
 DB 3967 AACAAATTCACTGCTAAGAGGCTGACAGACACAGATGGAAACCTTAGAAGACGA 4026
 QY 337 GlnCysGluPheGluArgLysPheAspGlyThrThrLeuGlyLeuLeuHisPro 356
 DB 4027 GTGAATTAAGTTTTCGCGCGCCAGAAAT-----CACCTT 4059
 QY 357 ValAspProIleValGlyLysProGlyTyrCysLeuValArgLeu----- 371
 DB 4060 -----GAGCTGGGAGGTTTGTGACAGATGCGGACAGCTCAGAC 4101
 QY 372 -----GlyMetThrThrGlyArgLeuGlnSerGly----- 381
 DB 4102 AAGACTGTGAGGTCAGCCGGAATGAAGTGTGTGATTCGAGAGATGTCG 4161
 QY 382 -----ValAsnThrLeuGlnGlyPheLysGlu----- 390
 DB 4162 GAATCTTCCATATCGTACCAAGCACTTGTGTTTGAGGAGATGATGAGTGCAT 4221
 QY 391 -----AspLysArgAsnLysValThr 397
 DB 4222 GTGTGCTTTTGGAGTCATGTGCAGATACGGCTGATGGCCCCCAACAAATACAA 4281
 QY 398 ProValLeuLysLeuAsnTyr--GlyProTyrSerSerTyrAla----- 411
 DB 4282 GCGTGTGATATCATATCTTATCTGACAGTATTAATTTCCGCGCCGCTGCTCGG 4341
 QY 412 -----ProHis-----T 414
 DB 4342 ACACGTGTTTACATGATGATCCTCATCGATATCTCGATATGTGAAAGAAATGGTGTAT 4401
 QY 414 TyrAspSerThrPheAlaAsnLysSer--Lys-AspAspSerAspLeuIleTyrSerThr 432
 DB 4402 GTGACAGACATATTTGGGCGCTGTCCCAAGTGAAGAGATGACTATATCTTCATTGC 4461
 QY 433 TyrGlyLysAspSerAspLysProSerAspPheSerIleHisGluPheLeuAlaThrCys 452
 DB 4462 CACCCCTGTACAGAAATCCCAACCAACCAACTACAGAGTGTGTACAGAAAGATG 4521

QY 453 GlnAspTyrProTyrVal-----MetAlaAspSerLeuLeuAspValLeuThrLysGly 470
 DB 4522 CTGGAACAAGCGCTTTCAGAGAGATCATTAACGATATTAAGACATCTTCAAAAGCG 4581
 QY 471 GlyHisSerArgThrLeuGlnGluMetGluMetSerLeuProGluAspGlyHisThr 430
 DB 4582 AACGAACAGAGGTCACGAGTGCACGAGTTCCTATTTTGAAGAGATTTCTGCGCT 4641
 QY 491 ArgThrLeuAspPheLysLys-----LysGluMetGlnGlnIleThrGluValGluProGly 509
 DB 4642 AATGTGTGAAGAAACATTAAGAACTAGAACAA-----GAGAGAGAAAGAAAGAA 4695
 QY 510 ArgLeuAspSerSerThrGlnAsp-ArgLeuIleAlaLeuLysValThrAsnPheG 529
 DB 4696 AAGGAAGAGAGTCTGACAGAGTGAAGTCTCCGAGGCGAGTCAAGGTGACA----- 4747
 QY 529 yValProValGluValPheAspSerGluGluIlePheGlnLysLysLeuAspG 549
 DB 4748 -----GCMAAAATGCGAAGAAAGAA----- 4768
 QY 549 uThrThrArg-----LeuLeu-ArgGluLeuGlnGluValag 561
 DB 4769 -ACAACAAGAAAGCAACAAACAAAGACGATTAAGCCGCGCAACAAAGAAAGACC 4827
 QY 561 LysAsnGluArgLeuSerThrArgProProGlyAsnMetLysCys 575
 DB 4828 AGCATGCCCAATGTTTCCAAAGACGCTGTGCAAGACGTGATATC 4871

RESULT 9
 US-08-557-128-3
 ; Sequence 3, Application US/08557128
 ; Patent No. 5849524
 ; GENERAL INFORMATION:
 ; APPLICANT: KONDO, Keiji
 ; APPLICANT: KAJIWARA, Susumu
 ; APPLICANT: MISAWA, No. 5849524hiko
 ; TITLE OF INVENTION: TRANSFORMATION SYSTEMS FOR THE YEAST
 ; TITLE OF INVENTION: CANDIDA UTILIS AND THE EXPRESSION OF HETEROLOGOUS GENES
 ; NUMBER OF SEQUENCES: 40
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 3000 K Street, N.W., Suite 500
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20007-5109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/557,128
 ; FILING DATE: 25-JAN-1996
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: WO PCT/JP95/01005
 ; FILING DATE: 25-MAY-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 7-129287
 ; FILING DATE: 28-APR-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 6-285823
 ; FILING DATE: 26-OCT-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 6-135015
 ; FILING DATE: 25-MAY-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BENT, Stephen A.
 ; REGISTRATION NUMBER: 29,768
 ; REFERENCE/DOCKET NUMBER: 49441/108
 ; TELECOMMUNICATION INFORMATION:


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Db 283 GAGGACAGAGAAAGAGCA-----GAGAAAG-----309
Qy 124 SerLeuAlaLysGlnGluValGlnGlnThrPro-----Leu 136
Db 310 -----GCAAGACAGAGAGGAGAGAAAGAGAGCTCCGCTCAGTCCGAAACAGAGACTA 363
Qy 137 GlnGlnAlaLeuGlnGlnLeuMetArgGlnLeuGlnArgLysAspProSerAlaIlePhe 156
Db 364 CAACACATTGCTACTCTCTCATCGAGAGACTTCCTCATACAGATACGCTCAGCGCTT 423
Qy 157 SerPheProValThrAspPheIleAlaProGlyTyrSerMetIleIleLysIlePheMet 176
Db 424 CTACACCTCTTAAAGAGTCCAGTCCAGGACCAACATTAATCTGATCAAGAAACAGAG 483
Qy 177 AspPheSerThrMetLysGlnLysIleLysAsnAsnAspTyrGlnSerIleGlnGlnLeu 196
Db 484 GATCTGAAGACCATCAACAGATGCTCAGACGACGATACAGACCAATCTTGACCTG 543
Qy 197 LysAspAsnThrLysLeuMetCysThrAsnAlaMetIleTyrAsnLysProGluThrIle 216
Db 544 GAGAGGAGATCTTGCTGATGTTTGGCAATGCCATCATGACACAGACCGGAGCGAT 603
Qy 217 TyrTyr-----LysAlaAlaLysLysLeuLysSerGlyMetLysIle 232
Db 604 ATCTACAGTGGACCAAGAGATGACCGGAACTTGAACAAGCTCATCGAGCTTTAAC 663
Qy 232 uSerGlnGlnArgIleGlnSerLysLysGlnSerIleAspPheMetAlaAspLeuGlnLys 252
Db 664 GAGAGTAATATGATACAGCTTACAGCTCAAGAAAGATGAAGAACGCTGATTAACG 723
Qy 252 eThrArgLysGlnLysAspGlyThrAspThrSerGlnSerGlyLysGlyCysTr 272
Db 724 GTATTGTAG-----TG 735
Qy 272 pGlnArgGlnArgGlnAspSerGlyAspAlaGlnAlaIleAspLysSerProSer-- 291
Db 736 GTATGTACAAAGGGGTGTCTTCTCAACCTCTTTCATGTGTGAGTCAAAAGCAGCT 795
Qy 292 -----LysGlnAsnLysLysLysAspLysAspMetLeuGlnAspLysPheLysSer 308
Db 796 TCTGCTCTTGAATCTAAGACCGACTCTTCCGAATGCTTGAAGAACTTTTCAGAGCA 853

RESULT 11
US-09-535-008-74
; Sequence 74, Application US/09535008
; Patent No. 6465629
; GENERAL INFORMATION:
; APPLICANT: Wong, Alexander K.C.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.-F.
; TITLE OF INVENTION: BRG1 IS A TUMOR SUPPRESSOR THAT IS MUTATED IN PROSTATE
; FILE REFERENCE: 2318-259
; CURRENT APPLICATION NUMBER: US/09/535,008
; CURRENT FILING DATE: 2000-03-23
; EARLIER APPLICATION NUMBER: U.S. 60/125,806
; EARLIER FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 74
; LENGTH: 5477
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (75)..(5021)
; FEATURE:
; NAME/KEY: conflict
; LOCATION: (1780)
; OTHER INFORMATION: GenBank Accession No. 6465629 U29175 shows a C at this
; OTHER INFORMATION: position (position 1784 in GenBank) rather than
; OTHER INFORMATION: the G shown here.
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FEATURE:
; NAME/KEY: allele
; LOCATION: (26)
; OTHER INFORMATION: Polymorphism of either T or C in this noncoding
; OTHER INFORMATION: region.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (1583)
; OTHER INFORMATION: Polymorphism of A or G resulting in a silent
; OTHER INFORMATION: mutation.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (1598)
; OTHER INFORMATION: Polymorphism of T or C resulting in a silent
; OTHER INFORMATION: mutation.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (1892)
; OTHER INFORMATION: Polymorphism of A or G resulting in a silent
; OTHER INFORMATION: mutation.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1445)..(1453)
; OTHER INFORMATION: Insertion of 9 basepairs as compared to SEQ ID
; OTHER INFORMATION: NO:1.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4507)..(4508)
; OTHER INFORMATION: Deletion of CNG between these basepairs as
; OTHER INFORMATION: compared to SEQ ID NO:1 (basepairs 4499-4501 of
; OTHER INFORMATION: SEQ ID NO:1).
US-09-535-008-74

Alignment Scores:
Pred. No.: 1,66e-10 Length: 5477
Score: 192.50 Matches: 82
Percent Similarity: 38.68% Conservative: 53
Best Local Similarity: 23.50% Mismatches: 107
Query Match: 6.26% Indels: 107
DB: Gaps: 16

US-09-687-230a-2 (1-589) x US-09-535-008-74 (1-5477)
Qy 2 G1LysLysHisLysLysHis-----LysSerAspLysHisLeuTyrGlnGluTyrVal 19
Db 4182 GGCTCCCGCCACCGCAAGAGGTGACTACAGCACTCA---CTGACGGAAGCACTGG 4238
Qy 20 GlnLysProLeuLysLeuValLysValGlyGlyAsnGlnValThrGlnLysSerThr 39
Db 4239 CTCAGACCTGTAAGGCCATC-----4259
Qy 40 GlySerSerLysHisAspSerSerLeuPheGlu---AspLysAsnAspHisAspLysHis 58
Db 4260 -----GAGGAGGCGACGCTGAGAGATTCGAAGAGAGAGCTCCGCGAAGAA 4307
Qy 59 LysAspArgLysArgLysLysArgLysGlyGlnLysGlnLysProGlnGlnLys 78
Db 4308 TCATCAGGAAGGCCAAGCAGACAGGAGCGCGCTCTCCACCCGACACAGC---4364
Qy 79 GlyArgLysArgArgValLysGlnAspLysLysLysArgAspArgAspArgValGln 98
Db 4365 -----ACCGCAGCGCCGACAGAGCAGAGCAAGAAAGCAAGAAAGCGCGCGG 4418
Qy 99 AsnGlnAlaGlnLysAspLeuGlnCysHisAlaProValArgLysAspLysProGln 118
Db 4419 CCGGCTGCGAGAA-----CTCTCCCTTAAC 4445
Qy 119 LysPro-----LeuThrSerSerLeuAlaLysGlnGlnGln 130
Db 4446 CCACCCAACTCACCAGAAAGATGAAGAAGATTGATGCCGATCACTACAAAGAGC 4505
Qy 131 ValGlnGlnThrProLeuGlnGlnAlaLeuAsnGlnLeuMetArgLysGlnGlnArgLys 150
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Db 4506 AGCAGTGCAGCTCAGCTCAGGAGGTCTTCATCCAGCTGCC-----TCGCGAAG 4556
Qy 151 AspProSerAlaPhePheSerPheProValThrAspPheIleAlaProGlyTyrSerMet 170
Db 4557 GAG-----CTGCCGAGTACTACGAG 4577
Qy 171 IleIleIleHisProMetAspPheSerThrMetLysGluLysIleLysAsnAsnAspTyr 190
Db 4578 CTATCCGCAAGCCCGGAGCTTCAAGAGATTAAGGCGCATTCGCAACCAACATAC 4637
Qy 191 GlnSerIleGluLysLysLysAspAsnPheLysLysMetCysThrAsnAlaMetIleTyr 210
Db 4638 CGCAGCTCTCAACGCTTGAAGAGAGAGCTCATCTCTGCTGCGAAGCGACGACCTTC 4697
Qy 211 AsnLysProGluThrIleTyrTyrTyrLysAlaLysLysLysLysLysSerGlyMetLys 230
Db 4698 AACCTGAGGAGCTCTCTGATCTTAAGAACTCC----- 4730
Qy 231 IleLysSerGlnLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 250
Db 4731 ATGCTCTTGAGTGGCTTCCAGAGCTGCGCGCAAAATCCAG----- 4775
Qy 251 GlnLysThrArgLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 270
Db 4776 -----AAGCAGGATGAC-----AGTGAAGCGCAGAGAGT--- 4805
Qy 271 CysTrpGlnArgLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 290
Db 4806 -----GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4853
Qy 291 SerLysGlnLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 307
Db 4854 TCCGTCAAATGAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 4913
Qy 308 -----SerrAsnLys 311
Db 4914 GGCCGCGCGCGCGCGCGAGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4973
Qy 312 GlnArgLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 320
Db 4974 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4997
RESULT 12
US-09-535-008-70
; Sequence 70. Application US/09535008
; Patent No. 6465629
; GENERAL INFORMATION:
; APPLICANT: Wong, Alexander K.C.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.-F.
; TITLE OF INVENTION: BRL1 IS A TUMOR SUPPRESSOR THAT IS MUTATED IN PROSTATE
; TITLE OF INVENTION: AND OTHER CANCER TYPES
; FILE REFERENCE: 2318-259
; CURRENT APPLICATION NUMBER: US/09/535,008
; CURRENT FILING DATE: 2000-03-23
; EARLIER APPLICATION NUMBER: U.S. 60/125,806
; EARLIER FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 70
; LENGTH: 5480
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (75)..(5024)
; NAME/KEY: conflict
; LOCATION: (1780)
; OTHER INFORMATION: Genbank Accession No. 6465629 U29175 shows a C at this
; OTHER INFORMATION: position (position 1784 in Genbank) rather than
; OTHER INFORMATION: the G shown here.

NAME/KEY: allele
LOCATION: (26)
OTHER INFORMATION: Polymorphism of either T or C in this noncoding
OTHER INFORMATION: region.
FEATURE:
NAME/KEY: allele
LOCATION: (1583)
OTHER INFORMATION: Polymorphism of A or G resulting in a silent
OTHER INFORMATION: mutation.
FEATURE:
NAME/KEY: allele
LOCATION: (1598)
OTHER INFORMATION: Polymorphism of T or C resulting in a silent
OTHER INFORMATION: mutation.
FEATURE:
NAME/KEY: allele
LOCATION: (1892)
OTHER INFORMATION: Polymorphism of A or G resulting in a silent
OTHER INFORMATION: mutation.
FEATURE:
NAME/KEY: misc feature
LOCATION: (4245)..(4253)
OTHER INFORMATION: Insertion of 9 basepairs as compared to SEQ ID
OTHER INFORMATION: NO:1.
US-09-535-008-70
Alignment Scores:
Pred. No.: 2,44e-10 Length: 5480
Score: 191.00 Matches: 83
Percent Similarity: 40.06% Conservative: 54
Best Local Similarity: 24.27% Mismatches: 113
Query Match: 6.22% Indels: 92
Gaps: 17
US-09-687-230A-2 (1-589) x US-09-535-008-70 (1-5480)
Qy 2 GlnLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 19
Db 4182 GGCTCCCGCCGCGCGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4238
Qy 20 GlnLysProLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 39
Db 4239 CTCAGACCCCTGAAGGCCATC----- 4259
Qy 40 GlySerSerGlyHisAspSerSerLysLysLysLysLysLysLysLysLysLysLys 58
Db 4260 -----GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4307
Qy 59 LysAspArgLysArgLysLysLysLysLysLysLysLysLysLysLysLysLysLys 78
Db 4308 TCATCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4364
Qy 79 GlnArgLysArgLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 98
Db 4365 -----ACCGCGAGCGCGCGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4418
Qy 99 AsnGlnAlaGlnLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 118
Db 4419 CCGCTGCGCGAGAA-----CTCTCCCTTAAC 4445
Qy 119 LysPro-----LysThrSerSerLysLysLysLysLysLysLysLysLysLysLys 137
Db 4446 CCACCACTCTACCAAG-----AGATCAAGAGATTCGATGCTGATCAAG 4496
Qy 138 GlnAlaLysAsnGlnLysLysLysLysLysLysLysLysLysLysLysLysLysLys 157
Db 4497 TACAAGACAGCAGCAGTGGAGCTCAGCTCAGC-----GAGGTCTTCATCCAG 4544
Qy 158 PheProValThrAspPheIleAlaProGlyTyrSerMetIleIleLysHisProMetAsp 177
Db 4545 CTGCCCTCGCGAAGAGCTG-----CCCGATCACTACAGCTCATCCGCGCGCTGAGC 4601
Qy 178 PheSerThrMetLysGlnLysLysLysLysLysLysLysLysLysLysLysLysLysLys 197

[illegible]

Db 4647 -----CTGCCCGAGTACTAGACCTCATC 4670
Qy 173 LysHisProMetAspPheSerThrMetLysGluLysIleuysAsnAnaAspTyrGlnSer 192
Db 4671 CGCAGCGCCGTCGACTTCAAGAAATTAAGAGCGCATTTCCCAACCAACTGACGAGC 4730
Qy 193 IleGluLysLeuLysAspAsnPhelLysLeuMetCysThrAnaIleuLysAsnLys 212
Db 4731 CTCACGACCTAGAGAGAGAGCGTCATGCTCTGTGCCAGAAAGCAGACCTCAACCTG 4790
Qy 213 ProGluThrIleTyrTyrLysAlaAlaLysLeuLeuHisSerGlyMetLysIleLeu 232
Db 4791 GAGGCTCCCTCGATCTAGAGACTCC-----ATCGTC 4823
Qy 233 SerGlnGluArgIleGlnSerLeuLysGlnSerIleAspPheMetAlaAspLeuGlnLys 252
Db 4824 TTGCAGTCGCTCTTCCACGAGGTCGGCAGAAATCCAG-----4862
Qy 253 ThrArgLysGlnLysAspGlyThrAspThrSerGlnSerGlyLysAspGlyCysTrp 272
Db 4863 -----AAGGAGATGAC-----AGTAGGCGCAGAGAGT-----4892
Qy 273 GlnArgGluArgLysAspSerGlyAspAlaGluAlaHisAlaPheLysSerProSerLys 292
Db 4893 -----GAGGAGGAGAGAGAGGCGCAGAGAGAGCTCCGATCCGATCTCGGTCGTC 4946
Qy 293 GluAsnLysLysLys-----AspLysAspMetLeuLysAspLysPheLys-----307
Db 4947 AAGTAGAATCAAGCTTGGCCGAGAGAGAGACAGACGCGCTGAAGGCGCGCGG 5006
Qy 308 -----SerAnaLysLeuLysArg 313
Db 5007 CGGCGCGCCAGCCGAGGCTCCCGACCGACCGCGCTCGTAGTACGATGACAGTGAAGAG 5066
Qy 314 GluGlnGluGlnLeuAspArg 320
Db 5067 GAACAAGAGAGAG--GACCGC 5084
RESULT 14
US-08-227-536-1
Sequence 1, Application US/08227536
Patent No. 5658784
GENERAL INFORMATION:
APPLICANT: Eckner, Richard
APPLICANT: Ewen, Mark
APPLICANT: Livingston, David
TITLE OF INVENTION: NUCLEIC ACID, ENCODING TRANSCRIPTION
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
STREET: Ten Post Office Square
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/227,536
FILING DATE: 14-APR-1994
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Williams Ph.D., Kathleen A.
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: DPCI-308XX
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-2290
TELEFAX: (617) 451-0313
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 9046 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
FEATURE:
NAME/KEY: CDS
LOCATION: 1200..8441
US-08-227-536-1
Alignment Scores:
Pred. No.: 6.2e-10 Length: 9046
Score: 190.50 Matches: 130
Percent Similarity: 33.44% Conservative: 83
Best Local Similarity: 20.41% Mismatches: 249
Query Match: 6.20% Indels: 175
Gaps: 26
US-09-687-230A-2 (1-589) x US-08-227-536-1 (1-9046)
Qy 38 SerThrGlySerSerGlyHisAspSerLeuPheGluAspLysAnaAspLys 57
Db 4065 TCTACTAGTACGACAGAGAGAAATTTCTCAGCGCATTCGTCAGAG-----CAGCCT 4115
Qy 58 HisLysAspArgLysArgLysLysLysLysLysLysLysLysLysLysLysLysLys 77
Db 4116 TCCAGAGAGTGAAGATGAGAGGCCAAATGGAAGTGATCAACAGAACAGAGATACG 4175
Qy 78 LysGlyArgLysArgArgValLysGluAspLysLysLysLysLysLysLysLysLys 97
Db 4176 CAGCCGAGAGATATTCAGAGTCTAAAGTGAAGCTGTAATGGAATCTACCGAAACA 4235
Qy 98 GluAsnGluAlaGluLysAspLeuGlnCysHisAlaProValArgLeuAspLeuProPro 117
Db 4236 GAA--GAGGAGAGCCTGAGTTAAATACTGAATAAAGAGAGAGAGAGAGAGAGT 4292
Qy 118 GluLysProLeuThrSerLeuAla-----LysGlnGluValGluGln 133
Db 4293 ACTTCAGCTACCCAGATCTCCGCTCCAGACAGTCAAGAAAGAAATTTCAACACA 4352
Qy 134 ThrProLeuGlnGluAlaLeuAsnGlnLeuMetArgGlnLeuGlnArgLysAspProSer 153
Db 4353 GAAGAACTACGACGAGCTGATGCCAACATTCAGAGCACTTACCGTCAGATCCAGAA 4412
Qy 154 AlaPhe---PheSerPheProValThrAspPheIle-----AlaProGlyTyrSerMet 170
Db 4413 TCCCTCCCTTGTGTCACCTGTGACCTCAGACTTTAGGAATCCCTGATTTCTTGAT 4472
Qy 171 IleIleLysHisProMetAspPheSerThrMetLysGluLysIleuysAsnAnaAspTyr 190
Db 4473 ATTGTGAAGAGCCCTGATCTTTCTACCATTAAGAGAGTACAGCTGACAGTAT 4532
Qy 191 GlnSerLysGlnGluLysAspAsnPhelLysLeuMetCysThrAnaIleuLys 210
Db 4533 CAGGAGCCCTGCGCATGTATCGATGATTTGGCTTATGTTCAATATGCTGTTATAT 4592
Qy 211 AsnLysProGluThrIleTyrTyrLysAlaAlaLysLysLeuLeuHisSerGlyMetLys 230
Db 4593 AACGGAAAAACATCAGCGGTATCAAAATCTGCTCAAGCTC-----TGTGAG 4640
Qy 231 IleLysSerGlnGluArgIleGlnSerLeuLysGlnSerIleAspPheMetAla-----248
Db 4641 GTCTTTGAACAGAA--ATTGACCAAGTATGCAAGCCTTGATGATCTGTGCAAGA 4697
Qy 249 -----AspLeuGlnLysThrArgLysGln 256
Db 4698 AAGTTGAGTCTCTCCACAGACACTGTGTGCTACGGAACAGTGTGACAAATACCT 4757
Qy 257 LysAspGlyThrAspThrSerGlnSerGlyLysAspGlyGlyCys-----271

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Db 4758 CGTATCCCACTTTTACAGTACAGAACAGTATCTTCTGTGAGAGTCTTCAAT 4817
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Qy 272 ---TrrGlnArgGluArgSerGlyAspAlaGluAlaIlePheLysSerPro 290
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Db 4818 GAGATCCAGAGGCGGACGCTTCTTGGGGATGACCTTCCAGCCTCAAACTACATA 4877
      ||| ||| ||| |||
Qy 291 SerIleGluAsn---LysLysLysAspLysAspIleLeuGluAspLysPhe---Lys 307
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Qy 308 SerAsnLeuGluArgGluGluGluLeu----- 318
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Qy 327 -----GlyLysLeuThrArgArgLeuVal 334
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Db 5058 AAGTTTCTGCTAAAGGTGCCATCTACAGACTTGGACCTTTCTAGAGAAATCGTGTG 5117
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Qy 335 AsnSerGlnCysGluPheGluArgArgLysProAspGlyThrThrLeuGlyLeuLeu 354
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Db 5118 AATGACTTTCTGAGGCGACAGAAATCACCCTGATCAGAGAGGTCATCTTGAAGTACT 5177
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Qy 355 HisProValAspProIleValIleGluProGlyLysLysValArgGluGlyMetThr 374
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Db 5331 GTTCAAGAGTATGGCTGATGCTGACCTCCACCAACAGAGAGATATATCTTAC 5390
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Qy 443 ---PheSerIleHisGluPheLeuAlaThrCys-----GlnAspTyrProTyrVal 458
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Db 5391 CTCGATAGTGTCTTCTTCCGCTTAATGCTTGAAGATGACGATCATATGAAATC 5450
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Qy 459 MetAlaAspSerLeuAspValLeuThrLysGlyLysIleSerArgThrLeuGlnGlu 478
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Db 5451 CTAAAT---GGATATTTAGATATGTCAGAAATTAAGTTACACA----- 5492
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Qy 479 MetGluMetSerLeuProGluAspGluGlyHisThrArgThrLeuAspThrGlyLysGlu 498
      ||| ||| ||| |||
Db 5493 -----ACAGGCGCATATTTGGCGATGTCACCAAGTAGAGGA 5528
      ||| ||| ||| |||
Qy 499 MetGluGlnIleThrGluValIleGluProProGlyArg----- 510
      ||| ||| ||| |||
Db 5529 GATGATTTATCTTCATTCCTGATCCATCTCTGACCAAGAAATACCAAGCCAGGACTG 5588
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Qy 511 -----LeuAsp----- 512
      ||| ||| ||| |||
Db 5589 CAGGAATGTACAAAAAATGCTGACAAAGCTGATCAGAGCGATATTCATGACTAC 5648
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Qy 513 -----SerSerThrGlnAspArgLeuIleAlaLeuLysAlaValThrAsn 527
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Db 5649 AAGGATATTTTAAACAAGCTACTGAAATGATTTAACAGTGCAAAGAAATGCTTAT 5708
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Qy 528 PheGlyValProValIleValIlePheAspSerGluGluIlePheGlnLysLysLeu 547
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Db 5709 TTC-----GAGGATTTCTGCCCCAATGTTCTG 5738
Qy 548 AspGluThrThrArgLeuLeuArgGluLeuGlnGluAlaGlnAsnGluArg 564
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Db 5739 GAAGAAAGC-----ATTAAAGAACTGAAACAGAGAGAAAGAGAGA 5780
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RESULT 15
PCT-US95-04682-1
Sequence 1, Application PC/TUS9504682
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: NUCLEIC ACID ENCODING TRANSCRIPTION
TITLE OF INVENTION: FACTOR P300 AND USES OF P300
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Weingarten, Schurigin, Gagnebin & Hayes
STREET: Ten Post Office Square
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04682
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 5
FILING DATE: 14-April-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Holliday C. Heine, Ph.D.
REGISTRATION NUMBER: 34,346
REFERENCE/DOCKET NUMBER: DPCI-308X999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-2290
TELEFAX: (617) 451-0313
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 9046 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHEICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1200..8441
PCT-US95-04682-1

Alignment Scores:
Pred. No.: 6.2e-10 Length: 9046
Score: 190.50 Matches: 130
Percent Similarity: 33.44% Conserves: 83
Best Local Similarity: 20.41% Mismatches: 249
Query Match: 6.20% Indels: 175
DB: 5 Gaps: 26

US-09-687-230A-2 (1-589) x PCT-US95-04682-1 (1-9046)
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 Db 4236 GAA---GAGGAGAACACTGAGCTTAAACCTGAATTAAGAGAGAGAAAGCAGCAAGT 4292
 QY 118 GluLysProLeuThrSerSerLeuAla-----LysGlnGluValGlnGln 133
 Db 4293 ACTTCAGCTACCCAGCTATCTCCGCTCCAGAGACGTCAAGAAAGATTTTCAACCA 4352
 QY 134 ThrProLeuGlnGluAlaLeuAsnGlnLeuMetArgLysGlnArgLysAspProSer 153
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 QY 154 AlaPhe---PheSerPheProValThrAspPheLe-----AlaProGlyTyrSerMet 170
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 QY 171 IleIleLysHisProMetAspPheSerThrMetLysGluLysIleLysAsnAspTyr 190
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 Db 4641 GTCCTTGAACAAAGA---ATTGACCAAGTATGCAAAAGCCTTGATCTGTGGCAGA 4697
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 QY 327 -----GlyLysLeuThrArgArgLysVal 334
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 QY 335 AsnSerGlnCysGluPheGluArgLysArgLysProAspGlyThrThrLeuGlyLeuLeu 354
 Db 5118 AATGACTTTCGAGGCGACAGAAATCACCTGAGTCAAGAGAGTCACTGTTAAGTAGTGT 5177
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 Db 5178 CATGCTTCTGACAAACCGTGGA-----GTAAACCAAGCATGATAA 5219
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 QY 548 AspGluThrThrArgLeuLeuArgGluLeuGlnGluAlaGlnAsnGluArg 564
 Db 5739 GAAGAAAGC-----ATTAGGAACCTGAAACAGAGAGAAAGAGAGA 5780

Search completed: November 27, 2003, 01:13:18
 Job time : 167 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 27, 2003, 00:55:13 ; Search time 35 Seconds

(without alignments)
3103.917 Million cell updates/sec

Title: US-09-687-230A-2

Perfect score: 3073
Sequence: 1 MGKKHKHKKDKHLYEYVE.....PGNMICLLGPSSEKICLLNK 589

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 673684 seqs, 18443283 residues

Total number of hits satisfying chosen parameters: 673684

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB.pep.*
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- 18: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2972.5	96.7	718	10	US-09-764-864-1579 Sequence 1579, App 1579
2	798.5	26.0	199	10	US-09-764-864-1166 Sequence 1166, App 1166
3	215	7.0	221	9	US-09-925-301-946 Sequence 946, App 946
4	210.5	6.8	2442	14	US-10-109-886-10 Sequence 10, App 10
5	205	6.7	1572	12	US-10-116-275-179 Sequence 179, App 179
6	198	6.4	2441	14	US-10-109-886-8 Sequence 8, App 8
7	187	6.1	1647	11	US-09-824-574-4 Sequence 4, App 4
8	183	6.0	580	10	US-09-764-864-1160 Sequence 1160, App 1160
9	181.5	5.9	898	15	US-10-043-487-277 Sequence 277, App 277
10	179.5	5.8	801	15	US-10-146-473-42 Sequence 42, App 42
11	167.5	5.5	680	12	US-10-102-143-19 Sequence 19, App 19
12	164.5	5.4	3051	12	US-10-144-194A-62 Sequence 62, App 62
13	162.5	5.3	665	11	US-09-820-843A-107 Sequence 107, App 107
14	160.5	5.2	240	10	US-09-764-864-1168 Sequence 1168, App 1168
15	158	5.1	779	12	US-10-144-194A-86 Sequence 86, App 86

16	155	5.0	636	12	US-10-032-585-7132 Sequence 7132, App 7132
17	153	5.0	947	15	US-10-293-822-1 Sequence 1, App 1
18	150	4.9	1938	15	US-10-171-311-164 Sequence 164, App 164
19	150	4.9	1945	11	US-09-927-597-2 Sequence 2, App 2
20	150	4.9	1972	12	US-10-341-434-103 Sequence 103, App 103
21	150	4.9	1972	15	US-10-171-311-162 Sequence 162, App 162
22	150	4.9	1979	11	US-09-927-597-4 Sequence 4, App 4
23	149.5	4.9	1087	12	US-10-080-608A-12 Sequence 12, App 12
24	149.5	4.9	1087	12	US-10-370-685-101 Sequence 101, App 101
25	149.5	4.9	1312	12	US-10-393-602-148 Sequence 148, App 148
26	149	4.8	439	12	US-10-354-804-5 Sequence 5, App 5
27	148.5	4.8	578	15	US-10-137-418A-3 Sequence 3, App 3
28	148.5	4.8	1390	15	US-10-137-418A-2 Sequence 2, App 2
29	148.5	4.8	1881	12	US-10-032-585-7666 Sequence 7666, App 7666
30	148	4.8	1104	15	US-10-128-714-3262 Sequence 3262, App 3262
31	148	4.8	1353	15	US-10-128-714-8262 Sequence 8262, App 8262
32	146	4.8	735	12	US-10-144-194A-109 Sequence 109, App 109
33	146	4.8	784	12	US-10-144-194A-108 Sequence 108, App 108
34	146	4.8	843	12	US-10-144-194A-84 Sequence 84, App 84
35	142.5	4.6	128	10	US-09-764-864-1571 Sequence 1571, App 1571
36	142.5	4.6	1170	12	US-10-341-434-95 Sequence 95, App 95
37	142.5	4.6	1979	15	US-10-205-823-419 Sequence 419, App 419
38	142	4.6	556	12	US-10-144-678A-1005 Sequence 1005, App 1005
39	142	4.6	556	12	US-10-294-025-1005 Sequence 1005, App 1005
40	142	4.6	556	14	US-10-012-896-1005 Sequence 1005, App 1005
41	141	4.6	505	9	US-09-815-242-11317 Sequence 11317, App 11317
42	141	4.6	505	11	US-09-820-843A-12 Sequence 12, App 12
43	140	4.6	137	10	US-09-764-864-1581 Sequence 1581, App 1581
44	139.5	4.5	774	12	US-09-949-029-126 Sequence 126, App 126
45	139	4.5	1703	10	US-09-801-368-340 Sequence 340, App 340

ALIGNMENTS

RESULT 1
US-09-764-864-1579
Sequence 1579, Application US/09764864
Patent No. US20020132753A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT23
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1792
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1579
LENGTH: 718
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (52)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (99)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-864-1579

Query Match 96.7%; Score 2972.5; DB 10; Length 718;
Best Local Similarity 99.1%; Pred. No. 2.4e-221; Indels 1; Gaps 1;
Matches 573; Conservative 4;
Db 3 KKHKHSDKHLVEYVEKPLKLVKVGNEVELSTGSGHDSLFEDKNDHKDKRK 62
70 KKHKHSDKHLVEYVEKPLKLVKVGNEVELSTGSGHDSLFEDKNDHKDKRK 129
QY 63 KKHKHSDKHLVEYVEKPLKLVKVGNEVELSTGSGHDSLFEDKNDHKDKRK 122
130 KKHKHSDKHLVEYVEKPLKLVKVGNEVELSTGSGHDSLFEDKNDHKDKRK 189

RESULT 5
US-10-116-275-179
; Sequence 179, Application US/10116275

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RESULT 6
US-10-109-886-8
Sequence 8, Application US/10109886
Publication No. US20020119499A1
GENERAL INFORMATION:
APPLICANT: TANABE SEIYAKU CO. LTD.
APPLICANT: TANIGUCHI, Tomoyaasu
APPLICANT: MIKIZAKI, Junko
TITLE OF INVENTION: METHOD FOR IDENTIFYING OR SCREENING AGONIST AND
FILE REFERENCE: TANIGUCHI-6
CURRENT APPLICATION NUMBER: US/10/109,886
CURRENT FILING DATE: 2002-04-01
PRIOR APPLICATION NUMBER: 09/514,247
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: PCT/JP98/03734
PRIOR FILING DATE: 1998-08-24
PRIOR APPLICATION NUMBER: JP231084/1997
PRIOR FILING DATE: 1997-08-27
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patencin version 3.0
SEQ ID NO 8
LENGTH: 2441

```

TYPE: PRT
ORGANISM: mouse
US-10-109-886-8

Query Match 6.4%; Score 198; DB 14; Length 2441;
Best Local Similarity 19.9%; Pred. No. 6.4e-06;
Matches 139; Conservative 93; Mismatches 219; Indels 248; Gaps 29;

QY 32 NEVTELTSSGSHSSIFEDKNDHDKKRRKKRKKGGKQIPDEEGRKRRKED--- 88
DB 971 NRVPTSTVTAETS--QQPGPVMLEMTETVQTDABEPRESKGEPRSEMEEDLQ 1028
QY 89 -KKKSDRDRENAEAKDLQCHAPVRLDLPPEKPLTSSLAKEVEQT----- 134
DB 1029 GSGVKEETITTEKSEPR-----MEVEKKEPEVKEVEKEEENSSNDTASQSTSPS 1079
QY 135 -----PLOBALNQLMKROLQKOPSAF-FSPVYTDFT--APGYSMTIKHPMDFSTM 181
DB 1080 QPRKKIKFPEBELRQALPTEALYRQDPESLPFRQPVDPOLGIPDYFDIVKQMDLSTI 1139
QY 182 KKKIKNDYQSIIEBKDNFKLMCTNAMIYKPEITYYKAAKLLHSGMKLISQRIQSLK 241
DB 1140 KKKLDTGQYQEPWQYVDVRLMENNAMLNKRKTSRYKFKSKL---AEVFEQD-IDPVM 1194
QY 242 QSIDFMADLQKTRKQKQDGT-----SOSGEDGCGW---QERE 277
DB 1195 QSLQVCGG---KRYERSPQTLCCYKQKQCTIPRDAVYSQNRHYHCGKCFTEIQGENV 1250
QY 278 DSGDAEHAFAKSPSKENKKDKMLIEDKPKSNMLE-----REQEOL----- 318
DB 1251 TLGD-----DPSQPTTISKQDFEKK-KNDTLDPRPFVDCKEGKRMHQICVLHYDII 1302
QY 319 -----DRIVEEG-----GKTLRLVNSQCEPERKRPDGTTLGLLHP 356
DB 1303 WPSGFVCDNCLKTKGRPRKKNKSAKRLQTTRLNHLIEDRVNKKFLRRQN-----HP 1353
QY 357 VDPVIGEPGYCLVRLGWTGTRLSQGVNTLQGFEDKKNKVPVL---YLVNGPYASYAPH 413
DB 1354 -----EAGEVFAVRVAVSS-----DKTVEKFKPKSKSFVDSGEMSESPFY 1392
QY 414 -----YDSTFANISKDSOLI-----YSTYGEDSDLPSDFSIEHFLAT 451
DB 1393 RTKALFAFEIADVGVCFGMHVDTLIAHPIQGCYVSIYLD-----SIHFRPR 1444
QY 452 C-----QDYPYMAADSLDVLTKG-----HSTTLQEME 480
DB 1445 CLRTAVVHEILIGYLEVYKLVVYTAHIMACRPSGSDYIFHCHPRDQKIPKPRQLQEWY 1504
QY 481 MSIPDEGHTRLDYGKEMQITEVEPRRLDSTODRLALKAVTNFVGVVEVDFDEEA 540
DB 1505 KKKLDRKAFARIINDYDI-----FKQANERLITSAKELPYF-----EG 1543
QY 541 EIFOKKLDFTTRRLRELQEAQNER-----LSTRPPGN 572
DB 1544 DFWPNVLEES---IKELQEEERKKESTASSETPGS 1579

RESULT 7
US-09-824-574-4
Sequence 4, Application US/09824574
Publication No. US20030077800A1
GENERAL INFORMATION:
APPLICANT: Rouleau, Natalie
APPLICANT: Moilanen, Anu-Maarit
APPLICANT: Palvimo, Jorma J.
TITLE OF INVENTION: Aripa Gene and Protein
FILE REFERENCE: 2630-109
CURRENT APPLICATION NUMBER: US/09/824,574
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4

LENGTH: 1647
TYPE: PRT
ORGANISM: Homo sapiens
US-09-824-574-4

Query Match 6.1%; Score 187; DB 11; Length 1647;
Best Local Similarity 23.1%; Pred. No. 2.6e-05;
Matches 77; Conservative 53; Mismatches 118; Indels 86; Gaps 14;

QY 7 KKKSDKLYEEYVEKPKLVKVGNEVTELTSSGSHSSIFEDKNDHDKKRRKKR 66
DB 1372 RHRKEVDYSDLTETKQWLKALIEGTLEIEI-----BEVROKSSKRRKRD 1416
QY 67 KKEGKQIPGEKRRKRRRVEDKKKDRDRENAEAKDLQCHAPVRLDLPPEKPLTSSLAKE 125
DB 1417 SDAGSSTPTTS---TNSRDQDSKQKQKGRPPAEK-----LSBNPNLYK-- 1460
QY 126 AKQEEVQTPLOEALNQLMKROLQKOPSAFSPVYTDFTIAPGYSMTIKHPMDFSTMKEKI 185
DB 1461 -KKKKIVDAVIKYKDSGSRQLS---EVFIQPSRREL-PEYVELIRKVPDFKIKERI 1514
QY 186 KANDYQSIIEBKDNFKLMCTNAMIYKPEITYYKAAKLLHSGMKLISQRIQSLKSID 245
DB 1515 RNHKYSINDLEKDVMLLCMAQTFNLEGLIYEDS-----IVLQSVFTSVROKIE 1565
QY 246 FMADLQKTRKQKQDGTDSOSGEDGCGQREERDSGAHAFAKSPSKENKK--DKDML 303
DB 1566 -----KEDD-----SEGEES-----EEEGEGESSESRSVYKIKLGRKEKAQ 1606
QY 304 DKFK-----SNMLEREQOLDR 320
DB 1607 DRUKGRRRPSRGRAPKPVVSDDSSEDEGE-DR 1639

RESULT 8
US-09-764-864-1160
Sequence 1160, Application US/09764864
Patent No. US20020132753A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT223
CURRENT APPLICATION NUMBER: US/09/764,864
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1792
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1160
LENGTH: 580
TYPE: PRT
ORGANISM: Homo sapiens
US-09-764-864-1160

Query Match 6.0%; Score 183; DB 10; Length 580;
Best Local Similarity 19.8%; Pred. No. 1.2e-05;
Matches 102; Conservative 73; Mismatches 155; Indels 184; Gaps 19;

QY 9 KSDKHLVEEYVEKPKLVKVGNEVTELTSSGSHSSIFEDKNDHDKKRRKKR 68
DB 53 RNDKYAGEEGMIDMKLMFRNARHYNE-----GSQYVYDA--HILEKLKEKREKL 102
QY 69 GEKQIIGEKEGRRKRVKEDKKKDRDRENAEAKDLQCHAPVRLDLPPEKPLTSSLAKE 128
DB 103 G--PLPDDDD-----MASPKLILSR-----KSGISPK 127
QY 129 EEVEQTPLOEALNQLMKROLQKOPSAFSPVYTDFTIAPGYSMTIKHPMDFSTM 181
DB 128 KSKYMTPMQKLVNEVAVKNTYDKGRRLSALFLPLPSSEL-PDYLYLTKKPMDEKI 186
QY 182 KKKIKNDYQSIIEBKDNFKLMCTNAMIYKPEITYYKAA-----KKLLHS----- 227
DB 187 RSHMANKYQDIDISVDEDFVMFNNACTYNEPESLIVKDALVHVKVLETRRLDEGDEDS 246

QY 228 ---GKILSGERISQSLKOSI----- 244
DB 247 HVENVTLLIQELLJHNLFEVSVMSHODDEGRCSYSDSLAEIPAVDPNFPNPKPLTFDILIRKNV 306
QY 245 -----DPMADLOKTRKQKOGTDTSGSGEGGCMQ-----ERESGD---- 281
DB 307 ENNRVRLDLFOGHMEFVLERARRMRTD--SEIYEDAVELQOFPKIRDLCKNGELILLS 365
QY 282 -----AEAHAFKSPSKENKK-KDKMLEDKFSNNLREOOLDRIVKESGKLTIRLVN 335
DB 366 PALSYTTKHLANDVEKERKELKREIREDLTKREERKEKESDSSGAAGLSGHRHTYS 425
QY 336 SOCFERRRRKPDGTTTGLLHPVPDIVEPG-----YCLVRLGWTGTRLOSQVNTLQG 387
DB 426 QDCSFKN-----SMHYGVGVYVPEAPAMLQPHIVICIERLMEDS-----AGEKMLYG 472
QY 388 -----FKEDKRNKVTPTV 399
DB 473 CMFERNETFLATRKFLKEKEVFKSDYNNKV-PV 505

RESULT 9

US-10-043-487-277
; Sequence 277, Application US/10043487
; Publication No. US20030055220A1
; GENERAL INFORMATION:
; APPLICANT: HYBRIGENICS
; APPLICANT: Pierre, LEGRAIN
; TITLE OF INVENTION: Protein-protein interactions between Shigella flexneri polypeptid
; FILE REFERENCE: B4778A
; CURRENT APPLICATION NUMBER: US/10/043,487
; PRIOR FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 561
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 277
; LENGTH: 898
; TYPE: PRT
; ORGANISM: Shigella flexneri
US-10-043-487-277

Query Match 5.9%; Score 181.5; DB 15; Length 898;
Best Local Similarity 21.0%; Pred. No. 2.9e-05;
Matches 118; Conservative 81; Mismatches 195; Indels 167; Gaps 21;

QY 6 KKHSDKHLVEEYVEKPLKLVKVGNEVTELTSGSGHDSILFEDKNDHKDKRRKK 65
DB 380 KKRRTGTTCVCDYLRPHKSIHRRRTDPMVTLSSILESTINDMRDLPTNYPTFTPVNAYV 439
QY 66 RKKGGEQIQEEEGKRRKRYKEDKKR--DRDR-----VENEAKDLOCHAPVR-- 112
DB 440 VVDYKTI--TRPMLOTLRENVKRLKLPSEEFREHLELIYKNSATYNGPGLSLQIS 496
QY 113 ---LDLPEKPLTSSLAKEEVEQTPLQELNLMQLQKQPSAF----- 155
DB 497 QSMULDCEK-----LKEKEDLARLEKAINPL--LDDDDVAASFLIDNIIVTKMAA 547
QY 156 -----FSPFVTDPIAGYSMIILKHPMDSFTMKETIKNDYQSIIEELKDNFKLMCTNAMI 209
DB 548 VPDSWFPHRPNVKKFVPDYKVIIVNPMDELITIKNSIKHKYQSRSEFLDDVNIILANSYK 607
QY 210 YNKPEITTYKAAKLLHSGMKILISQ--ERISQSLK-----QSIDPMADLQ 251
DB 608 YNGPESQYTKQELIVNVCYQTLTEYDEHLTQLEKQICTAKAALAEAELESIDPMTPGP 667
QY 252 KTRKQKDGDTDSOS---GEDGCGMOREREDS--GDAEAHAFKSPSKENKKKQD----- 300
DB 668 YTFQPPDLVDYNTSLMSNRDASVFQDESNNWSVLDISAPPEKQYTOBEGEDGDLADEEB 727
QY 301 -----MLDEKFSNNLREOOLDRIVKESGKLTIRLVNQSCEFERRRKPDGTTT 350

DB 728 GTVQOPQASVLYEDLLMS---EGEDEDEBAGSDEBDN-----PFSAIQLSESGSDDVG 779
QY 351 LGLLHVDPDPIVGBPGVCLVRLGWTGTRLOSQVNTLQFKEDKRNKXTPTVY----- 401
DB 780 SGGIRKQPMW-----LGE--NT-----RDMENESMWSYBGDGBASH 817
QY 402 -----LNYGYSSVAPH---YDSTPANI----- 421
DB 818 GLEDSNISGSYSEPPPKSNTQDTSTFSISIGYVRSREBDEBDEBQSRGSPVLSQVHLSE 877
QY 422 SKDSDPLITYSTGDESDLPD 442
DB 878 DEEDSEDFHSIAG-DSDLSD 897

RESULT 10

US-10-146-473-42
; Sequence 42, Application US/10146473
; Publication No. US20030108888A1
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew
; APPLICANT: Gout, Ivan
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Gure, Ali
; APPLICANT: Chen, Yao-Tsang
; APPLICANT: Old, Lloyd
; TITLE OF INVENTION: Breast Cancer Antigens
; FILE REFERENCE: L00461/70130(JRV)
; CURRENT APPLICATION NUMBER: US/10/146,473
; PRIOR FILING DATE: 2002-05-15
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 42
; LENGTH: 801
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-473-42

Query Match 5.8%; Score 179.5; DB 15; Length 801;
Best Local Similarity 27.2%; Pred. No. 3.5e-05;
Matches 67; Conservative 36; Mismatches 90; Indels 53; Gaps 10;

QY 110 PVRLDPEKPLTSSLAKEEVEQTPLQEL--NOLMRQLOKQPSAF--FSPFVTD 163
DB 323 PIK---PPRKDLPPDSQQHQSSKKGKLSQLKHCNGLIKELLSKKAAYAMPFYKPV-DA 378
QY 164 IAPG---YSMIILKHPMDSFTMKETIKNDYQSIIEELKDNFKLMCTNAMIYNKETIYYKA 220
DB 379 SALGLHDYDITKHPMDSLTVKRNKENDYDQAEPAADVRLMFSCTYNNPDDVAM 438
QY 221 AKKL-----LHSGMKILISQERISQSLKOSIDPMADLOKTRKQKOGTDTDSOS 265
DB 439 ARKLDQVFEFYAKWDEPLBGPPLVSTAMPGL-----AKSSSESSSES 485
QY 266 GEDGCGWQEREDSGDAEAHAFKSPSKENKKKDKMLEDKFSNNLREOOLDRIVKES 325
DB 486 SSSSESESEBDEBDEE-----EBESSSDSEEB--RAHRLAELOEL-RAVHEQ 533
QY 326 GKKLTR 331
DB 534 LAAISO 539

RESULT 11

US-10-102-143-19
; Sequence 19, Application US/10102143
; Publication No. US20030185851A1
; GENERAL INFORMATION:
; APPLICANT: Soldati, Dominique
; APPLICANT: Meisner, Markus
; TITLE OF INVENTION: Tet transactivator system

```
FILE REFERENCE: 04630/016001
CURRENT APPLICATION NUMBER: US/10/102,143
CURRENT FILING DATE: 2003-01-21
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19
LENGTH: 680
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
US-10-102-143-19

Query Match
Best Local Similarity 35.0%; Score 167.5; DB 12; Length 680;
Pred. No. 0.00024;
Matches 36; Conservative 24; Mismatches 42; Indels 1; Gaps 1;

123 SSLAKOE-VEQTPLOEALNQLMRQLQKDPASAFSPVTDPIAGYSMTIKHPMDFSTM 181
Db 564 AGRAKEGKLRASLSKAOIALSLTEKSSSWFRFPVSEAPDYEVVRRPIDISTM 623

Qy 182 KKKKNDYOSIEBLKDNFKLMCTNAMIYKPEYIYKAAKTL 224
Db 624 KKGNRNGDYRTKEAFQEDLLMFQNCRVNSPTIYKYADEL 666

RESULT 12
US-10-144-194A-62
Sequence 62, Application US/10144194A
Publication No. US20030215809A1
GENERAL INFORMATION:
APPLICANT: Origene Technologies Inc
TITLE OF INVENTION: Regulated Breast Cancer Genes
FILE REFERENCE: 3U 103 R1
CURRENT APPLICATION NUMBER: US/10/144,194A
CURRENT FILING DATE: 2002-06-12
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn version 3.0
SEQ ID NO 62
LENGTH: 3051
TYPE: PRT
ORGANISM: Homo sapiens
US-10-144-194A-62

Query Match
Best Local Similarity 5.4%; Score 164.5; DB 12; Length 3051;
Pred. No. 0.0035;
Matches 126; Conservative 102; Mismatches 249; Indels 153; Gaps 24;

Qy 16 EBYVEKPLKVLKVGNEVTELTSGSGHDSLFEDKNDHDKHDKRRKKKGEKQIPG 75
Db 278 EEFSDLC-----PVEIKYTYEHNHLILNKDVQSSSQKKSITDKGEKPKDS 328

Qy 76 BEKGRKRRRYKE-----DKKKRDRRVENE--AEKDLQCHAPYRLDLPPEKPLTSS 124
Db 329 NEKERKKEKEKEKEKEKEDHKSSEDYQKDEKQAKEKEVE-----SLKLPSEK---N 379

Qy 125 LAKOEVEQTPLOEALNQLMRQLQKDPASAFSPVTDPIAGYSMTI--KHPMDFSTM 181
Db 380 SNRAKATVEGT-----KED-----FSLIDSDVDGJLDITIVSSVHTSDLSSEF 419

Qy 182 KE-----KIKNDYOSIEBLKDNFKLMCTNAMIYKPEYIY-----YK 219
Db 420 EEDTEEBVYVTSDSNEBGEITSDDE--EKNKQNTKTQTSSESGKTSVHAAYVHKPYL 476

Qy 220 AAKLLHSGMKILSOERIOS-----LKOSIDPMADLOKTRKQKQKQDTQSOGEDG 270
Db 477 YSKYISDSDELTVEQRQSIKAKEKERLLRQIN-REKLEBKQKQKQKESKTKQGG 535

Qy 271 CWQREEDSG--DAEAAAFKSPSKENKKDKOM-LEDKFKSNLLEQOQLDRIVKES 325
Db 536 RSVVDLESSSTKSLPEPKAARIKAVLKERKVLKVKVALSKKQKDSRVNEENSKKQOYEB 595
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Qy 326 GGLTRRLVNSQCEFERRRPDGTTTGLLHPVDPIVEBQYCLVRLGWTGRLQSGVNTL 385
Db 596 DSKETLK-TSEHC--EKETISSSEKELKHVH---AKSEPSKPARRLSESLHVDENKNES 648
Qy 386 QCFKEDKRNKVTPLYLYNAGPYSYAPHDSTFANISKQDSLDLYSTYGEDSPLPDFSI 445
Db 649 KIEREHRRTSTPVI-----MEGVQESTDTRDVRQVERSSI----- 665
Qy 446 HEFLATCODYPYVMADSLDLVLTGSHSRTLQEMEMSLPEDEGHTRTLDTGKEMEQITTEV 505
Db 686 -----CTEEPQKQKSTL-----KNEGLKKDDETHLKSLLKKEVYSSK 725
Qy 506 EPPGRDSSSTODRLIAK-----AVTNFQVPEVDFDSEBAEYFQKKLDETTLLBELQ 559
Db 726 EKPERKTPSEDKL-SVKHKYKGDGMKGTDETELHSSSEKGLKVEENIQOSQOTKLSSD 784
Qy 560 AONERLSTRPPGMICLLG-----PSEKCI 585
Db 785 DKTERKSKHNRERKLSVLGDKGKPVSEYII 814

RESULT 13
US-09-820-843A-107
Sequence 107, Application US/09820843A
Publication No. US2003003963A1
GENERAL INFORMATION:
APPLICANT: Council of Scientific and Industrial Research
TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEIN
FILE REFERENCE: Q63915
CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.0
SEQ ID NO 107
LENGTH: 665
TYPE: PRT
ORGANISM: Plasmodium falciparum
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: hypothetical protein
NAME/KEY: misc feature
OTHER INFORMATION: g1|3845248
US-09-820-843A-107

Query Match
Best Local Similarity 5.3%; Score 162.5; DB 11; Length 665;
Pred. No. 0.00056;
Matches 67; Conservative 57; Mismatches 107; Indels 97; Gaps 12;

Qy 6 KKHSDGHLVEEYVEKPLKVLKVGNEVTELTSGSGHDSLFEDKNDHDKHDKRRKK 65
Db 295 KKETDKTHLEB-----ENEIIEKE-----FSDKKQKQKQKQKQK 331

Qy 66 RKKGKQ-----IPGE- KGRKRRRYKEDKKGRDRVENEAKDLQCHAPYRLDLPPEK 120
Db 332 SKDTEKESKQIDIEKESKQDEKESKQDEKESKQDEKESKQDEKESKQDEKESKQDEKESK 390

Qy 121 LTSSLAQE-----EVEDTPLOEALNQLMRQLQKDPASAFSPVTDPIAGYSMTIIGHM 176
Db 391 KDTAKEKEKQDIEKESKQMEKLNKQNDKQKQDN----- 427

Qy 177 DFTMKKIKNDYOSIEBLKDNFKLMCTNAMIYKPEYIYKAAKLLHSGMKILSOER 236
Db 428 -----EK-KKNDKQDJDHND-----ENDM-----EE 449

Qy 237 IOSLKOSIDPMADLOKTRKQKQKQDTQSOGEDGQWQREBDSGDAEAAAFKSPSKENK 296
Db 450 IEBNDEDEDEDEBNKKKKKGGKNGENGENG--SENGENGENGENGENGENGENGEN 507

Qy 297 KQKMLEDKFKSNLLEQOQLDRIVK 324
Db 508 NENENENENGENENENENENENENENENENENENENENENENENENENENENENENENENEN 534
```

RESULT 14
US-09-764-864-1168
; Sequence 1168, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT23
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PAM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 1168
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-864-1168

Query Match 5.2%; Score 160.5; DB 10; Length 240;
Best Local Similarity 25.4%; Pred. No. 0.00019;
Matches 48; Conservative 33; Mismatches 59; Indels 47; Gaps 7;

QY 110 PVRLLDPPEKPLT--SSIAKQEEVEQTPLOEALNQLKROLQ-----RKDPASAFSPV 160
DB 3 PTR---PRKLSKRSKISPKSKYMTFMOQKNEVEAVKNTYDKRGRSLAIFLRPS 59
QY 161 TDFIAPGYSMIIGHMDFSTMKEKIKNDYQSIIEELKNFKNCTNMIYKDETIYKA 220
DB 60 RSEL-PPYVLTIKKPMMEKIRSHMANKYQDIDSWEDFVMMFNACTYNEPESLIYKD 118
QY 221 A-----KKLHS-----GKILSOERISQKOSIDFPAIDQKTRKQDGTDS 263
DB 119 ALVLHKKVLETRDLEGEDESHVNPVTLIQELIHLNLFVS-----MS 161
QY 264 QSGEDGCGW 272
DB 162 HODDEGRCY 170

RESULT 15
US-10-144-194A-86
; Sequence 86, Application US/10144194A
; Publication No. US20030215809A1
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies Inc
; TITLE OF INVENTION: Regulated Breast Cancer Genes
; FILE REFERENCE: 3U 103 R1
; CURRENT APPLICATION NUMBER: US/10/144,194A
; CURRENT FILING DATE: 2002-06-12
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: Patent version 3.0
; SEQ ID NO 86
; LENGTH: 779
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-144-194A-86

Query Match 5.1%; Score 158; DB 12; Length 779;
Best Local Similarity 18.4%; Pred. No. 0.0016;
Matches 120; Conservative 110; Mismatches 230; Indels 178; Gaps 29;

QY 3 KKHKKHSDKHLVEYVEKPL--KLVKVGNEV-----TELSTGSGGHDSSL 48
DB 235 KKKKKKKED--IFRRFPVAPLIPYPLITKEDINAIEEEDKRDLLISREISKPRDTH-KKL 291
QY 49 FEDKNDHDKKDKKKRKKKGGKQIPEEGKRRKRVKEDKKRDRPVNEAKLOCH 108
DB 292 EEKGGKKERKQIEKEREKRRERERERERERERERERERERERERERERERERERERER 350
QY 109 APVRLDLPPEKPLTSSIAKQEEVEQTPLOEALNQLKROLQKDPASAFSPVTDIAPGY 168

DB 351 RERERERERERKOKRDRDEDEDA---YERRKLEKLEKEA-----Y 393
QY 169 SMIKKPMDSSTMKKIKKNDYQ-SIEBKDNFKLCTNMIY-----NKPEITIY 218
DB 394 QERLKN---WEIRERKTRREYKAEAREERERERERERERERERERERERERERERERER 449
QY 219 KAAKLLHSGMKILSOERISQKSIDFPAIDQKTRKQDGT-----TSQSGDGG 270
DB 450 RGS-----ALQRLDRREKME--ADERDRKREKELEBIRORLLAEHPDDAE 497
QY 271 CWQREEDSGDAHAHAFKSPSKENKKDKMLDKFKSNLREBQGLDR----- 320
DB 498 LQRMQEAERRRQPIQOEPESEEESEKQEKKEK-REBPMEEEBEPQCLKPLRPI 556
QY 321 ---IKESGCKLTRLNVSQCEFERKRPDGTTLGL--HPVDPIVGEQYCLVRLGMT 374
DB 557 SSAPSVSSASGNAT-----PNTPEDESPCGIIIPHENSPOOQEEHRRPKIGLS 605
QY 375 TGRLOSGVNTLQGFKEKDKNKVTPVLYLNGPYSSYAPHYSTFANISKDSD----- 427
DB 606 ---LKGASNSPQGPNSVVRKLPV-----DSVFNNKFEDESDSDVRRKR 647
QY 428 LIYSTYGEDSDLPDSFSIH-----EFLATQD---YP--YVWADSLDLVLT 469
DB 648 LVPLDYGEDDKNATKGTVNTBEKRIKSLIEKIPAKPELFAVPLDWSIVDSIL----- 702
QY 470 GHSRFLQEMSLPDEGHTRTLDGKEMEQITVEPGRLDSSIODRLIALKATVNF 529
DB 703 -----MERRI-----RWINKKIIEYIGEBE-----ATLVDFVCSKVAH-S 738
QY 530 VPVEVFD-----SEEAIFOKLDEFTTLRLRELOEQ 561
DB 739 SPQSIIDVAMVLDEBAVFIVM---WRLLIYETEAR 773

Search completed: November 27, 2003, 01:10:19
Job time : 37 secs

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OM protein - protein search, using sw model

Run on: November 27, 2003, 00:37:26 ; Search time 22 Seconds

(without alignments)
1132.777 Million cell updates/sec

Title: US-09-687-230A-2

Perfect score: 3073
Sequence: 1 MGKKHKKKSKDKHLVEEYVE.....PGNNICLLGPSSEKCIILNK 589

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42110858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep.*
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4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PTUS.COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3073	100.0	589	US-08-942-008-2	Sequence 2, Appl1
2	685	22.3	159	US-08-747-562-10	Sequence 30, Appl1
3	210.5	6.8	2442	US-09-514-247A-10	Sequence 10, Appl1
4	198	6.4	2441	US-08-194-468-2	Sequence 2, Appl1
5	198	6.4	2441	US-08-961-739-2	Sequence 2, Appl1
6	198	6.4	2441	US-09-514-247A-8	Sequence 8, Appl1
7	192.5	6.3	1649	US-09-535-008-75	Sequence 75, Appl1
8	191	6.2	1650	US-09-535-008-71	Sequence 71, Appl1
9	191	6.2	1678	US-09-535-008-69	Sequence 69, Appl1
10	190.5	6.2	2414	US-08-227-536-2	Sequence 2, Appl1
11	190.5	6.2	2414	PCT-US93-04682-2	Sequence 2, Appl1
12	189.5	6.1	1646	US-09-535-008-67	Sequence 67, Appl1
13	188.5	6.1	1646	US-09-535-008-65	Sequence 65, Appl1
14	188.5	6.1	1681	US-09-535-008-77	Sequence 77, Appl1
15	187	6.1	1647	US-09-535-008-2	Sequence 2, Appl1
16	187	6.1	1682	US-09-535-008-73	Sequence 73, Appl1
17	181.5	5.9	1872	US-08-188-582-14	Sequence 14, Appl1
18	181.5	5.9	1872	US-08-646-715-14	Sequence 14, Appl1
19	181.5	5.9	1893	US-08-188-582-11	Sequence 11, Appl1
20	181.5	5.9	1893	US-08-646-715-11	Sequence 11, Appl1
21	153	5.0	947	US-09-418-780A-1	Sequence 1, Appl1
22	150.5	4.9	1312	US-08-687-080-51	Sequence 51, Appl1
23	149.5	4.9	1087	US-09-914-259-12	Sequence 12, Appl1
24	149.5	4.9	1312	US-08-592-126-148	Sequence 148, App
25	149.5	4.9	1312	US-09-168-595-148	Sequence 148, App
26	147.5	4.8	1588	PCT-US93-07261-11	Sequence 11, Appl1
27	147.5	4.8	1663	PCT-US93-07261-16	Sequence 16, Appl1

28	146.5	4.8	2662	US-09-595-684B-31	Sequence 31, Appl1
29	144	4.7	800	US-09-555-790A-2	Sequence 2, Appl1
30	144	4.7	1866	US-08-938-105-3	Sequence 3, Appl1
31	142	4.6	1898	US-08-056-200-94	Sequence 94, Appl1
32	142	4.6	1898	US-08-800-644-94	Sequence 94, Appl1
33	142	4.6	3248	US-08-353-700-1	Sequence 1, Appl1
34	142	4.6	3248	PCT-US95-16216-1	Sequence 1, Appl1
35	141.5	4.6	2482	US-08-328-254-6	Sequence 6, Appl1
36	140	4.6	1939	US-09-310-187A-1	Sequence 1, Appl1
37	138.5	4.5	765	US-08-663-112-2	Sequence 2, Appl1
38	138.5	4.5	885	US-09-914-259-10	Sequence 10, Appl1
39	138.5	4.5	1196	US-09-107-532A-3944	Sequence 3944, Ap
40	135	4.4	8991	US-08-714-741-32	Sequence 32, Appl1
41	133.5	4.3	1161	US-09-337-536-2	Sequence 2, Appl1
42	133	4.3	967	US-09-914-259-21	Sequence 21, Appl1
43	133	4.3	3878	US-09-914-259-11	Sequence 11, Appl1
44	132.5	4.3	1388	US-08-685-576-4	Sequence 4, Appl1
45	130.5	4.2	1404	US-08-801-308-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-08-942-008-2
; Sequence 2, Application US/08942008
; Patent No. 6131419
; GENERAL INFORMATION:
; APPLICANT: Basellmann, Sylvia
; TITLE OF INVENTION: Nucleotide Sequences that Encode
; TITLE OF INVENTION: Phosphatidylinositol-3' Kinase Associated Proteins and
; TITLE OF INVENTION: Uses Thereof
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ONYX Pharmaceuticals, Inc.
; STREET: 3031 Research Drive
; CITY: Richmond
; STATE: CA
; COUNTRY: USA
; ZIP: 94806
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/942,008
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gioceta, Gregory
; REGISTRATION NUMBER: 32,028
; REFERENCE/DOCKET NUMBER: ONYX1027
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 262-8710
; TELEFAX: (510) 222-9758
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 589 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-942-008-2
Query Match 100.0%; Score 3073; DB 3; Length 589;
Best Local Similarity 100.0%; Pred. No. 4,8e-262;
Matches 589; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 MGKKHKKKSKDKHLVEEYVEKPLKLVKGVNVEYTELSTSSGGHDSLFEDKXNDHDKKD 60
Db 1 MGKKHKKKSKDKHLVEEYVEKPLKLVKGVNVEYTELSTSSGGHDSLFEDKXNDHDKKD 60
Cy 61 RKRKRKKKKKQIPGEKRGKRRRVKEDKKKRDNDRVNEAKNDLQCHAPVRLDLPEKRP 120

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Db 61 RRRKKKKKKQKQIGEEKGRARRVKEKKKKRDRDVENAEKQLQCHAPRDLDPREK 120
Qy 121 LTSLAKOEVEQTPLOALNQLMRQLOKPSAFSPPTDFTAPGYSMITIKPMDSST 180
Db 121 LTSLAKOEVEQTPLOALNQLMRQLOKPSAFSPPTDFTAPGYSMITIKPMDSST 180
Qy 181 MKKIKKNNDDYOSIEELKDNFKLMCTNMTYKPEITTYKAKKLLHSGMKLLSQRISQL 240
Db 181 MKKIKKNNDDYOSIEELKDNFKLMCTNMTYKPEITTYKAKKLLHSGMKLLSQRISQL 240
Qy 241 KQSIDFMADLOKTRKQKQKGTDTSSQSGEDGCMQEREDSGDAEAHAFSPKSKKKKDXD 300
Db 241 KQSIDFMADLOKTRKQKQKGTDTSSQSGEDGCMQEREDSGDAEAHAFSPKSKKKKDXD 300
Qy 301 MLEDFKSNLNEREOQLDRIVKESGKLTRLVNSQCEFFRRKPDGTTTGLLHPVDPI 360
Db 301 MLEDFKSNLNEREOQLDRIVKESGKLTRLVNSQCEFFRRKPDGTTTGLLHPVDPI 360
Qy 361 VGEFGYCLVRLGTTTGRLOSGVNTLQGFKEKRNKVPVLVYNGPSSVAPHYDSTFAN 420
Db 361 VGEFGYCLVRLGTTTGRLOSGVNTLQGFKEKRNKVPVLVYNGPSSVAPHYDSTFAN 420
Qy 421 ISKDSDLIYSTYGEDSLPSPDFSIHEFLATCQDYPYVMAADSLDLVLTGSHSRLOEME 480
Db 421 ISKDSDLIYSTYGEDSLPSPDFSIHEFLATCQDYPYVMAADSLDLVLTGSHSRLOEME 480
Qy 481 MSLEDEGHTRTLDTGKMEQITEVEPPGRILDSITODRLIALKAVTNGVPEVDFSEEA 540
Db 481 MSLEDEGHTRTLDTGKMEQITEVEPPGRILDSITODRLIALKAVTNGVPEVDFSEEA 540
Qy 541 EIFQKKIDETRLRLRELOAONERLSTRPPGNMCLLGPSSSEKCLLNK 589
Db 541 EIFQKKIDETRLRLRELOAONERLSTRPPGNMCLLGPSSSEKCLLNK 589

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RESULT 2

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US-08-747-562-30
Sequence 30, Application US/08747562
Patent No. 6579697
GENERAL INFORMATION:
APPLICANT: WALLACH, David
APPLICANT: BOLDIN, Mark
APPLICANT: METT, Igor
APPLICANT: VAREFOLOREV, Eugene
TITLE OF INVENTION: MODULATOR OF TNF/NGF SUPERFAMILY RECEPTORS
TITLE OF INVENTION: AND SOLUBLE OLIGOMERIC TNF/NGF SUPERFAMILY RECEPTORS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,562
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05854
FILING DATE: 11-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 109,632
FILING DATE: 11-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 111,125
FILING DATE: 02-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.

```

```

REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH-15A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 159 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-747-562-30

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Query Match 22.3%; Score 685; DB 4; Length 159;
Best Local Similarity 91.3%; Pred. No. 1,2e-52;
Matches 136; Conservative 3; Mismatches 8; Indels 2; Gaps 2;

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Qy 274 REREDSGD-AEAHAFKSPKSKKKKKKMDKEDFKSNLNEREOQLDRIVKESGKLTTR 332
Db 5 RERERTLEVAEAHAFKSPKSKKKKKKMDKEDFKSNLNEREOQLDRIVKESGKLTTR 64
Qy 333 LVNSQCEFFRRKPDGTTTGLLHPVDPIVGEFGYCLVRLGTTTGRLOSGVNTLQGFKEBK 392
Db 65 LVNSQCEFFRRKPDGTTTGLLHPVDPIVGEFGYCLVRLGTTTGRLOSGVNTLQGFKEBK 124
Qy 393 RNKVTPLYLNL-YGPSSVAPHYDSTFAN 420
Db 125 RNKVTPLYLNL-YGPSSVAPHYDSTFAN 153

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RESULT 3

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US-09-514-247A-10
Sequence 10, Application US/09514247A
Patent No. 6365361
GENERAL INFORMATION:
APPLICANT: TANABE SEIYAKU CO. LTD.
APPLICANT: TANIGUCHI, Tomoyasu
APPLICANT: MIZUKAMI, Junko
TITLE OF INVENTION: METHOD FOR IDENTIFYING OR SCREENING AGONIST AND ANTAGONIST TO PPAR
FILE REFERENCE: TANIGUCHI=6
CURRENT APPLICATION NUMBER: US/09/514,247A
CURRENT FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: PCT/JP98/03734
PRIOR FILING DATE: 1998-08-24
PRIOR APPLICATION NUMBER: JP231084/1997
PRIOR FILING DATE: 1997-08-27
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.0
SEQ ID NO 10
LENGTH: 2442
TYPE: PRT
ORGANISM: human
US-09-514-247A-10
Query Match 6.8%; Score 210.5; DB 4; Length 2442;
Best Local Similarity 21.2%; Pred. No. 4.7e-09;
Matches 143; Conservative 80; Mismatches 213; Indels 239; Gaps 32;
Qy 36 ELSTGSGHDSLFEEDKND--HDKDKRRKKKKKKGEKQIPGEKGRKRRVKEK--- 88
Db 982 ETNSQCGPDPVPLEMKTETQAEDETEP-----PGSKGEPSEMMEDLQ 1028
Qy 89 --KKKRDREVENAEKDLQCHAPVLDLPPEKLTSLAKOEVEQT----- 134
Db 1029 ASQYKEETDIAEOKSE-----PMEVD--EKREVVVEKVEEESSSNGTASGTSPSQ 1079
Qy 135 -----PLQBALNQLMRQLOKPSAF-FSPPTVDFI--AGYSMITIKHPMDFTMK 182
Db 1080 PRKIFKPEBDRQMLMTLEALTRQDPESLPFROPVPOLGLPDIYKPNPDLSTIK 1139
Qy 183 EKIKNNDDYOSIEELKDNFKLMCTNMTYKPEITTYKAKKLLHSGMKLLSQRISQLQ 242
Db 1140 RKLDYGYQGFVWQVVDVWMLFNNAMLYNKRKTSRVYVFCSL-----AEVFEQ- 1194

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QY 243 SIDFMA-----DLQTRKQDGTDSQSGEDGCG-----MQREREDSGDA 282
DQ 1195 SLGCGCRKRYEFSPQTLCCYQKQCTIPRDAAYYSYQNRHYFCKCFTEIOGENVTGLD- 1253
QY 283 EAHAFKSPSKENKKKDKMLDEKFKSNLLE-----REGEOL----- 318
DQ 1254 -----DPSQPTTISKQFEEK-KNDTLDEPFVDCCKGKKNHQICVLHYDIIMPSGF 1306
QY 319 ---DRIVESG-----GKTRLVNSQCFERKRDGTTLGLHPVPIV 361
DQ 1307 VCDNCKKGTGRPKRKNFSARLQTRLGNHLEDRVNFRLRQN-----HP----- 1352
QY 362 GEPYCLVRLGTMTRQLSGVNTLQGFEDKRNKVTPLV-----YLYNGPYSSYAPH-YDST 417
DQ 1353 -EAEVFRVYVASS-----DKTVEYKPGMKSRFPVDSGEMSESPFYRTKAL 1396
QY 418 FANISKDSDLIY-----STYGEDSLPDS-----FSIHEFLATC---QDYPYVAD 461
DQ 1397 FAFEDIGVDVCFGMHVQEVGSDCPNTRRYVYSYLSDSIHFRPRCLRTAVYHEILIG 1456
QY 462 SLIDLVLTKG---GHSRTLOEMEMSLPEDEG-----HTRTLDYKMEQITEVEPPGRLD- 512
DQ 1457 YLEEVKKLGYVTGHI-----MACPSEBGDDYIFCHPPD-----QKIPKPKLOE 1501
QY 513 -----STODRLIALKAVTNFGVVEVFESEAEIRQKLD 549
DQ 1502 WYKMLDKAFARIINDYKDFKQATEDRLTSAXELPYF-----EGDFPNTVLEB 1551
QY 550 TTRLRLRELQEAONER 564
DQ 1552 S---IKELEOEER 1563

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RESULT 4
US-08-194-468-2
; Sequence 2, Application US/081944468
; Patent No. 5750336
; GENERAL INFORMATION:
; APPLICANT: Montminy, Marc R.
; TITLE OF INVENTION: ASSAYS FOR THE IDENTIFICATION OF
; TITLE OF INVENTION: COMPOUNDS WHICH INHIBIT ACTIVATION OF CAMP AND MITOGEN
; TITLE OF INVENTION: RESPONSIVE GENES
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Precy, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/194,468
; FILING DATE: 10-FEB-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)-546-4737
; TELEFAX: (619)-546-9392
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

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US-08-194-468-2
Query Match 6.4%; Score 198; DB 1; Length 2441;
Best Local Similarity 19.9%; Pred. No. 5.9e-08;
Matches 139; Conservative 99; Mismatches 219; Indels 248; Gaps 29;

QY 32 NEYTELSTGSSGHDSSLFEDKNDHKDKRRKKRKKGKQIPGEKGRKRRRYKED--- 88
DQ 971 NRPVPTSTVTSATSS--QQPGPDVPLMEKTEVQTDADAPPEFTESGGEERSEMEEDLQ 1028
QY 89 ---KKRRDRVENEAKDLQCHAPVRLDLPPEKPLTSLAKQBEVET----- 134
DQ 1029 GSSQVKEETDTTQKSEP-----MEVEKKKEVKEVEAKEEENSSNDTASQSTSPS 1079
QY 135 -----PLGEALNQLMRQLOKQDPSAF-PSFPTDIT--APGSMILKHPMDSTM 181
DQ 1080 QPRKKIFKPEELRQALPTEALYRDPESLPFRQVPDQLGIPDYFDIVKXNMDLSTI 1139
QY 182 KEKIKNNDYOSIEELKDNFLMCTNMTYNNKPEITYYKAKKLLHSGMKILSQERISLK 241
DQ 1140 KRKLDTGQYQEPBQYVDVRLMFRNNAVLNKRKTSRYVKFCSKL-----ASVFEQE-IDPYM 1194
QY 242 QSIDPMADLQKTRKQKQDGT-----SQSGEDGCGW---QERE 277
DQ 1195 QSLGCGC---RKYESPQTLCCYQKQCTIPRDAAYYSYQNRHYFCGKCFTEIOGENV 1250
QY 278 DSGDAEHAHAFKSPSKENKKKDKMLDEKFKSNLLE-----REGEOL----- 318
DQ 1251 TLGD-----DPSQPTTISKQFEEK-KNDTLDEPFVDCCKGKKNHQICVLHYDI 1302
QY 319 -----DRIVESG-----GKTRLVNSQCFERKRDGTTLGLHP 356
DQ 1303 WPSGFVCDNCKKGTGRPKRKNFSARLQTRLGNHLEDRVNFRLRQN-----HP 1353
QY 357 VDPVGEPRYCLVRLGTMTRQLSGVNTLQGFEDKRNKVTPLV-----YLYNGPYSSYAPH 413
DQ 1354 -----EAEVFRVYVASS-----DKTVEYKPGMKSRFPVDSGEMSESPFY 1392
QY 414 -----YDSFANISKDSDLI-----YSTYGEDSLPDSFSIHEFLAT 451
DQ 1393 RTALFAFEIDVDVCFGMHVQDGLALPHQIQGVYSYLD-----SIHFRPR 1444
QY 452 C-----QDYPYVADSLIDLVLTKG-----HSRTLOEME 480
DQ 1445 CLRTAVYHEILIGYLEVKKLVYTAHIAACPSBGDDYIFCHPPQKIPKPKLOEY 1504
QY 481 MSLEDEGHTRTLDYKMEQITEVEPPGRLDSTODRLIALKAVTNFGVVEVFESEEA 540
DQ 1505 KQMLDKAFARIINDYKDI-----FKQANEDRLTSAXELPYF-----EG 1543
QY 541 EIPQKLDETTRLRLRELQEAONER-----LSTRPPGN 572
DQ 1544 DFMPNTVLEBS---IKELEOEERKKKESTASSETPGS 1579

RESULT 5
US-08-961-739-2
; Sequence 2, Application US/08961739A
; Patent No. 6063583
; GENERAL INFORMATION:
; APPLICANT: Montminy, Marc R.
; TITLE OF INVENTION: Methods for Treating Diabetes Mellitus
; FILE REFERENCE: SALK1650-1
; CURRENT APPLICATION NUMBER: US/08/961,739A
; CURRENT FILING DATE: 1997-10-31
; EARLIER APPLICATION NUMBER: US 194,468
; EARLIER FILING DATE: 1994-02-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatcSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2441
; TYPE: PRT
; ORGANISM: Mus

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FEATURE:
NAME/KEY: VARIANT
LOCATION: (1) (2441)
OTHER INFORMATION: Xaa = Any Amino Acid
US-08-961-739-2

Query Match 6.4%; Score 198; DB 3; Length 2441;
Best Local Similarity 19.9%; Pred. No. 5.9e-08;
Matches 139; Conservative 93; Mismatches 219; Indels 248; Gaps 29;

QY 32 NEVELTSGSGHSSLFEDKNDHDKRKKRKKKKGEKQIPGEKGRKRRKED--- 88
DB 971 NRVPSTVTSATSS--QOPGPDVPMLEKTEVQTDABEPFESKGEPRSEMMEDLQ 1028
QY 89 ---KKKRRDRVENEAEKDLOCHAPVRDLPEPEKLTSSLAKEVEQT----- 134
DB 1029 GSSQVKEETDTTEQKSEP-----MEVEKKPEVKVAKEEENSNDTASQSTSPS 1079
QY 135 -----PLOEALNQLMRQLQRKDPSPAF-FSPVYDFI--APGYSMITIKHPMDFSTM 181
DB 1080 QPRKKIFKPEELRQALMPTLEALYQDPESLPFRQPVDPQLGIDYFDIVKPMDLSTI 1139
QY 182 KEKIKNDYOSIEELKDNFKLCTNMTYKPEITYYKAAKLLHSGMKILSOERISLK 241
DB 1140 KRKLDTQGYQEPWQYVDVRLMFNNAMLYNKRKTSRYKFCSKL---AEVFEQ-IPVM 1194
QY 242 QSIDPMADLQTRKQKGTDT-----SOSGEDGCGM---QRERE 277
DB 1195 QSLGCGG---RKYEFPQTLCCYQKQCTIPDAAYSYQNRVHFCGKCFTEIOGENV 1250
QY 278 DSGDAEHAAPKSPSKENKKDKMLDEKFSNNLE-----REOQL----- 318
DB 1251 TLGD-----DPSQPTTISKQFEKK-KNDTLDPEPFVDCKEGKGMQICVLHYDI 1302
QY 319 -----DRIVESG-----GKLTRELVNSQCEFERKRPDGTTLGLLHP 356
DB 1303 WPSGFVCNCLKTKGRPRKKNKFSAKRLQTRLGNHLEDVNNFLRRQN-----HP 1353
QY 357 VDPVIGBPGYCLVRLGWTGRLOSGVNTLQGFKEKKNKTPVL---YLVNGPYSSAPH 413
DB 1354 -----EAGEVPRVAVAS-----DKTVEKPRKMSRVSDEGSESESPY 1392
QY 414 -----YDSTFANISKDSDLI-----YSTYGEDSDLPSPFSIHEFLAT 451
DB 1393 RTKALFAFEEIDGVDFCFGMHVQDTALIAHQIQCVCYISYLD-----SIHFRPR 1444
QY 452 C-----QDYFYVMADSLVLTKG-----HSRTLQEME 480
DB 1445 CLRTAVYHEILIGLYEVKKLVYVTAHMACPSEGDYIFHCHPPDQIKPRKRLQEWY 1504
QY 481 MSLPEDEGHTRLDTGKEMEQITEVEPRGRLDSSQDRLIALKAVTNFVGVVEVDFSEEA 540
DB 1505 KKMULDRAFAERIINDYKDI-----FKQANEDRLTSAKELPYF-----EG 1543
QY 541 EIFOKLDETRLLRELOEAQNER-----LSTRPPGN 572
DB 1544 DFMPNVLEES---IKELQEEERKKESTAASETPEGS 1579

RESULT 6
US-09-514-247A-8
Sequence 8, Application US/09514247A
Patent No. 6365361
GENERAL INFORMATION:
APPLICANT: TANABE SEIYAKU CO. LTD.
APPLICANT: TANIGUCHI, Tomoyasu
APPLICANT: MIZUKAMI, Junko
TITLE OF INVENTION: METHOD FOR IDENTIFYING OR SCREENING AGONIST AND ANTAGONIST TO PPR
FILE REFERENCE: TANIGUCHI-6
CURRENT APPLICATION NUMBER: US/09/514, 247A
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: PCT/JP98/03734
PRIOR FILING DATE: 1998-08-24

PRIOR APPLICATION NUMBER: JP231084/1997
PRIOR FILING DATE: 1997-08-27
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patent version 3.0
SEQ ID NO 8
LENGTH: 2441
TYPE: PRT
ORGANISM: mouse
US-09-514-247A-8

Query Match 6.4%; Score 198; DB 4; Length 2441;
Best Local Similarity 19.9%; Pred. No. 5.9e-08;
Matches 139; Conservative 93; Mismatches 219; Indels 248; Gaps 29;

QY 32 NEVELTSGSGHSSLFEDKNDHDKRKKRKKKKGEKQIPGEKGRKRRKED--- 88
DB 971 NRVPSTVTSATSS--QOPGPDVPMLEKTEVQTDABEPFESKGEPRSEMMEDLQ 1028
QY 89 ---KKKRRDRVENEAEKDLOCHAPVRDLPEPEKLTSSLAKEVEQT----- 134
DB 1029 GSSQVKEETDTTEQKSEP-----MEVEKKPEVKVAKEEENSNDTASQSTSPS 1079
QY 135 -----PLOEALNQLMRQLQRKDPSPAF-FSPVYDFI--APGYSMITIKHPMDFSTM 181
DB 1080 QPRKKIFKPEELRQALMPTLEALYQDPESLPFRQPVDPQLGIDYFDIVKPMDLSTI 1139
QY 182 KEKIKNDYOSIEELKDNFKLCTNMTYKPEITYYKAAKLLHSGMKILSOERISLK 241
DB 1140 KRKLDTQGYQEPWQYVDVRLMFNNAMLYNKRKTSRYKFCSKL---AEVFEQ-IPVM 1194
QY 242 QSIDPMADLQTRKQKGTDT-----SOSGEDGCGM---QRERE 277
DB 1195 QSLGCGG---RKYEFPQTLCCYQKQCTIPDAAYSYQNRVHFCGKCFTEIOGENV 1250
QY 278 DSGDAEHAAPKSPSKENKKDKMLDEKFSNNLE-----REOQL----- 318
DB 1251 TLGD-----DPSQPTTISKQFEKK-KNDTLDPEPFVDCKEGKGMQICVLHYDI 1302
QY 319 -----DRIVESG-----GKLTRELVNSQCEFERKRPDGTTLGLLHP 356
DB 1303 WPSGFVCNCLKTKGRPRKKNKFSAKRLQTRLGNHLEDVNNFLRRQN-----HP 1353
QY 357 VDPVIGBPGYCLVRLGWTGRLOSGVNTLQGFKEKKNKTPVL---YLVNGPYSSAPH 413
DB 1354 -----EAGEVPRVAVAS-----DKTVEKPRKMSRVSDEGSESESPY 1392
QY 414 -----YDSTFANISKDSDLI-----YSTYGEDSDLPSPFSIHEFLAT 451
DB 1393 RTKALFAFEEIDGVDFCFGMHVQDTALIAHQIQCVCYISYLD-----SIHFRPR 1444
QY 452 C-----QDYFYVMADSLVLTKG-----HSRTLQEME 480
DB 1445 CLRTAVYHEILIGLYEVKKLVYVTAHMACPSEGDYIFHCHPPDQIKPRKRLQEWY 1504
QY 481 MSLPEDEGHTRLDTGKEMEQITEVEPRGRLDSSQDRLIALKAVTNFVGVVEVDFSEEA 540
DB 1505 KKMULDRAFAERIINDYKDI-----FKQANEDRLTSAKELPYF-----EG 1543
QY 541 EIFOKLDETRLLRELOEAQNER-----LSTRPPGN 572
DB 1544 DFMPNVLEES---IKELQEEERKKESTAASETPEGS 1579

RESULT 7
US-09-535-008-75
Sequence 75, Application US/09535008
Patent No. 6465629
GENERAL INFORMATION:
APPLICANT: Wong, Alexander K.C.
APPLICANT: Tavligian, Sean V.
APPLICANT: Teng, David H.-F.
TITLE OF INVENTION: BRG1 IS A TUMOR SUPPRESSOR THAT IS MUTATED IN PROSTATE
TITLE OF INVENTION: AND OTHER CANCER TYPES

Db 1665 EQEE-DR 1670

RESULT 10

US-08-227-536-2
Sequence 2, Application US/08227536

Patent No. 5658784

GENERAL INFORMATION:

APPLICANT: Eckner, Richard

APPLICANT: Ewen, Mark

APPLICANT: Livingston, David

TITLE OF INVENTION: NUCLEIC ACID, ENCODING TRANSCRIPTION

TITLE OF INVENTION: FACTOR P300 AND USES OF P300

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes

STREET: Ten Post Office Square

CITY: Boston

STATE: MA

COUNTRY: US

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/227,536

FILING DATE: 14-APR-1994

CLASSIFICATION: 436

ATTORNEY/AGENT INFORMATION:

NAME: Williams Ph.D., Kathleen A.

REGISTRATION NUMBER: 34,380

REFERENCE/DOCKET NUMBER: DFCI-308XX

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-2290

TELEFAX: (617) 451-0313

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 2414 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-227-536-2

Query Match 6.2%; Score 190.5; DB 1; Length 2414;
Best Local Similarity 20.4%; Pred. No. 2.7e-07;
Matches 130; Conservative 83; Mismatches 249; Indels 175; Gaps 26;

QY 38 STGSGHDSLFEDKNDHDKRRKKRKKGEKQIPGEGRKRRRVKEDKKRRDRV 97
DB 956 STSTEVNSQALIAEK---QPSQEVKMEAKMEVDQPEPADTQPEDISESKVEDCKMESTET 1012
QY 98 ENEMKLOQCAVPRDLPEKPLTSSLA---KOEVEQVPLQELANQLKROLQKQPS 153
DB 1013 E-ERSTELKTEIKKEEDPSTSATQSSAPQSQKKKIFKPEELLKQALMPTLEALYRQDPE 1071
QY 154 AF-FSPFVTDRI--APGYMTIKHPMDFTMKERIKNNDYOSIELKDNFKLMCTNMIY 210
DB 1072 SLPRQVDPDQLGIPDFIVKSPMDLSTIKRKLDTGQVPEPMQYVDIWMNNMMLY 1111
QY 211 NKPEITIIYKAAKKLLHSGMKLLSQERISLQKSIDFMA-----DIQKTRKQ 256
DB 1132 NKRTRSVYKYSKSL---SEVFEQE-IDPVMSGLGCGRKLESPQTLCCYKQOLCTIP 1186
QY 257 KDGCDTQSQSDGCG-----WQREBRESGDAEAHAFSPKKN-KKKDKMLDKF--K 307
DB 1187 RDAIYYSQNRHYHCEKCFNEIQGESVSLGDPSPQPTTIKKEQFSKKRNDTLLPELFE 1246
QY 308 SNNLEREOEOL-----DRIVKESG-----GKLTRELIV 334
DB 1247 CTBGRKMHQICVHLHETIWPAGFVDCCLKKSAKTRKKNKFSKAKRLPSTYLGTFLENRV 1306

QY 335 NSOCFEERRKPDGTTTLGLHPVDPYVGERGYCLVRLGTTGRLOSQVNTLQGFKEKDRN 394
DB 1307 NDFLRQNHPESEGEVTVRVVHSDKYVE-----VKGMARVDSG-EVASEF----- 1353
QY 395 KATPVLYLYNGPYSSAPHYDSTFANISKSDSLIY-----STYGBDSLPD----- 442
DB 1354 -----PYRTKA-----LFAPEIDGVLDLFCFGMHVQEGSDCPPNORRYISY 1397
QY 443 -FSIHEFLATC---QDYPYVADSLLDVLTKGHSRLQMEMSLPDEBHTRLDTGKE 498
DB 1398 LDSVHFEPKCLRTAVYHEILL-GYLEYVKQLGYT-----TSHIACPPSEG 1443
QY 499 MEDITEVEPRGR-----LD-----SSTODRLTALKAVTN 527
DB 1444 DDYIFHCHPDDQKIPKPKLQEWYKKMLDKAVSERIVHYDKDIFKQATERTLSAKELPY 1503
QY 528 FGVPVEVFESEBAEIPQKLDFTTRLRLRELQEAQNER 564
DB 1504 F-----EGDFWENVLEES---IKELQGEER 1527

RESULT 11

PCT-US95-04682-2
Sequence 2, Application PC/TUS9504682

GENERAL INFORMATION:

APPLICANT: NUCLEIC ACID ENCODING TRANSCRIPTION

TITLE OF INVENTION: FACTOR P300 AND USES OF P300

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes

STREET: Ten Post Office Square

CITY: Boston

STATE: MA

COUNTRY: US

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/04682

FILING DATE: 14-APR-1994

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/227,536

FILING DATE: 14-APR-1994

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Holliday C. Heine, Ph.D.

REGISTRATION NUMBER: 34,346

REFERENCE/DOCKET NUMBER: DFCI-308X999

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-2290

TELEFAX: (617) 451-0313

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 2414 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US95-04682-2

Query Match 6.2%; Score 190.5; DB 5; Length 2414;
Best Local Similarity 20.4%; Pred. No. 2.7e-07;
Matches 130; Conservative 83; Mismatches 249; Indels 175; Gaps 26;

QY 38 STGSGHDSLFEDKNDHDKRRKKRKKGEKQIPGEGRKRRRVKEDKKRRDRV 97
DB 956 STSTEVNSQALIAEK---QPSQEVKMEAKMEVDQPEPADTQPEDISESKVEDCKMESTET 1012

QY 98 ENEAKDLOQCHAPVRLDLPEKPLTSSLA---KQEEVEQTPLOEALNOLMOLQOROPS 153
Db 1013 E-ERSTELTEIKKEEEDQPSATQSSPAPQSSKKKIFKPEELRQALMPTLEALYRQDPE 1071
QY 154 AF-FSPVYPTFI--AFGSMITIKHMPDFTMKEXIKKNDYQSIIEBKONFKLMCTNAMY 210
Db 1072 SLFPRQVDPDQLGIPDYFPIVKS PMDLSTIKRLDYGQYQEPQYVDDIWMENNAWLY 1131
QY 211 NKPEITVYKAKKLLHSGMKILSGERIQSLKSIDEMA-----DLQTRKQ 256
Db 1132 NRTSRVYKICSKL---SEVFEDE-IDPMQSLGICCGKRLKESFOTLCCYQKOLCTIP 1186
QY 257 KQDITDSQSGEDGCG---WQEREDSGDAEAAFKSPSKEN-KKKDXMLEDKF--K 307
Db 1187 RDATVYSYQNRHYFCCEKCFNEIOGESVSLDDPSQPTTINKQFGRKNDITLDPELFE 1246
QY 308 SNNLEREQEOL-----DRIYEGS-----GKLTIRLY 334
Db 1247 CTCGRMHQICVLHHEIWPAGFVCDGLKKSARTKENKFSKRLPSTRLGTFLENRV 1306
QY 335 NSQCEFERRRKPDGTTTLGLHPVDPIVGEBOYCLVRLGMTTGRLOSGVNTLQGFKEKRN 394
Db 1307 NDPLRRONHPESGEVTVRVVHASDKTVE-----VKFGMARFVDSG-EKAESEF----- 1353
QY 395 KATPVLYLNGPYSSYAPHYDSTFANISKDSDLIY-----STYGEDSDLPSPD----- 442
Db 1354 -----PRTKA-----LEAFEDIGVDLCFGMHVQEGSCPPENQRRVYISY 1397
QY 443 -FSIHEFLATC---QDYPRVMASSLDLVLTGSHSRTLOEMWMSLPBEGHTTLDTGKE 498
Db 1398 LBSVHFHFRPKCLRTAVVHEILL-GYLEVYKKGIVT-----TGHIWACPPSEG 1443
QY 499 MEGITEVERPGR-----LD-----SSTORLALAKAVTM 527
Db 1444 DDITFHCPDQKIPKPKRLOEWYKXMDKAVSERIVHDKYIFKQATEDRLTSAKELPY 1503
QY 528 FGVPVEFVDESEAEIFOKKLDFTTLLRLRELQEAQNER 564
Db 1504 F-----EGDFWPNVLEES---IKELQEEBER 1527

RESULT 12
US-09-535-008-65
; Sequence 65, Application US/09535008
; Patent No. 6465629
; GENERAL INFORMATION:
; APPLICANT: Wong, Alexander K.C.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.-F.
; TITLE OF INVENTION: BRG1 IS A TUMOR SUPPRESSOR THAT IS MUTATED IN PROSTATE
; FILE REFERENCE: 2318-259
; CURRENT APPLICATION NUMBER: US/09/535,008
; CURRENT FILING DATE: 2000-03-23
; EARLIER APPLICATION NUMBER: U.S. 60/125,806
; EARLIER FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 65
; LENGTH: 1679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-535-008-65

Query Match 6.2%; Score 189.5; DB 4; Length 1679;
Best Local Similarity 22.2%; Pred. No. 1.9e-07;
Matches 80; Conservative 62; Mismatches 119; Indels 99; Gaps 17;

QY 2 GKXKXKH--KSDKHLVEYVEKPLKVLKVGNEVTELST-----GSS 42
Db 1370 GSHRRKEVDYSDLSLEKQWLK-----KITGKDIDHTASVARGLOPQGLQFCTRAK 1422
QY 43 GHDSLFFEDKND--HDKHKDRKRRKKRKKGKQIPGEEKGRRRRVKKKDRDRVENE 100

Db 1423 AIBEGTLEIEIEEVROKSSRKRRKSDAGSSTPTTS---TRSRDKDESKQKKGRRP 1479
QY 101 AERDLOQCHAPVRLDLPEKRP-LTSSIAKQEVQTPLOEALNOLMOLQORKDSAPFSFP 159
Db 1480 AER-----LSPNPNLTK---KMKKIVDAVIXYDSSSGQLS---EVFIQLP 1521
QY 160 VTFDIAFGYSMITIKHMPDFTMKEXIKKNDYQSIIEBKONFKLMCTNAMYKPEITYK 219
Db 1522 SRKEL-PEYTELRKRVDFKIKERIRNKHYSRLNDLEKDWMLLCQNAQTFNLBSGLIYE 1580
QY 220 AAKKLLHSGMKILSGERIQSLKSIDFMADLOKTRKQKQDITDSQSGEDGCGWQEREDS 279
Db 1581 DS-----IYLQSVFTSVRQKIE-----KEDD-----SGEES-----EEEEE 1612
QY 280 GDAAEAAFKSPSKENKK--DKDMLEDKF-----SNNLEREQEOLDR 320
Db 1613 GEEGEGSESESRVYKIKLGRKEKADRLKGRRRRPSGRAPVVSDDSEEOEE-DR 1671

RESULT 13
US-09-535-008-67
; Sequence 67, Application US/09535008
; Patent No. 6465629
; GENERAL INFORMATION:
; APPLICANT: Wong, Alexander K.C.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.-F.
; TITLE OF INVENTION: BRG1 IS A TUMOR SUPPRESSOR THAT IS MUTATED IN PROSTATE
; FILE REFERENCE: 2318-259
; CURRENT APPLICATION NUMBER: US/09/535,008
; CURRENT FILING DATE: 2000-03-23
; EARLIER APPLICATION NUMBER: U.S. 60/125,806
; EARLIER FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 67
; LENGTH: 1646
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-535-008-67

Query Match 6.1%; Score 188.5; DB 4; Length 1646;
Best Local Similarity 22.3%; Pred. No. 2.2e-07;
Matches 76; Conservative 52; Mismatches 112; Indels 101; Gaps 13;

QY 7 KHKSDKHLVEYVEKPLKVLKVGNEVTELSTGSSGHDSLFFEDKNDHKHDKRRKKR 66
Db 1372 RHRKEVDYSDLSLEKQWLKAIIEGTLEIEIE-----EYVQKSSRRKRD 1416
QY 67 KXGKQIPGEEKGRRRRVKKRDRVENEAKEDLOQCHAPVRLDLPEKRP----- 120
Db 1417 SDAGSSTPTTS---TRSRDKDESKQKKGRRPRAEK-----LSPNPNLTCKM 1462
QY 121 --LTSSLAQEVEQTPLOEALNOLMOLQORKDSAPFSFPVDTFIAFGSMITIKHMPD 178
Db 1463 KKIIVDAVIXYDSSSGQLSEVFIQLP---SRKE-----LPEYTELRKRVDF 1506
QY 179 STMKEXIKKNDYQSIIEBKONFKLMCTNAMYKPEITYKAKKLLHSGMKILSGERIQ 238
Db 1507 KIKERIRNKHYSRLNDLEKDWMLLCQNAQTFNLBSGLIYEDS-----IYLQSVFT 1557
QY 239 SLKQSIDFMADLOKTRKQKQDITDSQSGEDGCGWQEREDSGDAEAAFKSPSKENKKK- 297
Db 1558 SVRQKIE-----KEDD-----SEGES-----EEEBEGEGSESESRVYKIKL 1598
QY 298 -DKDMLEDKF-----SNNLEREQEOLDR 320
Db 1599 GRKEKQADRLKGGRRRPSGRAPVVSDDSEEOEE-DR 1638

RESULT 14

```
US-09-535-008-77
; Sequence 77, Application US/09535008
; Patent No. 6465629
; GENERAL INFORMATION:
; APPLICANT: Wong, Alexander K.C.
; APPLICANT: Tavigian, Sean V.
; APPLICANT: Teng, David H.-F.
; TITLE OF INVENTION: BGI IS A TUMOR SUPPRESSOR THAT IS MUTATED IN PROSTATE
; TITLE OF INVENTION: AND OTHER CANCER TYPES
; FILE REFERENCE: 2318-259
; CURRENT APPLICATION NUMBER: US/09/535,008
; CURRENT FILING DATE: 2000-03-23
; EARLIER APPLICATION NUMBER: U.S. 60/125,806
; EARLIER FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 77
; LENGTH: 1681
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-535-008-77

Query Match
Best Local Similarity 21.8%; Score 188.5; DB 4; Length 1681;
Matches 81; Conservative 59; Mismatches 111; Indels 121; Gaps 16;

QY 2 GKXKHKH-KSDKLYEYVEKPLKLVKYGNEVTELSGSSGHDSLPF----- 50
DB 1370 GSRHKEVDYDSLTKEQWLK-----KITGDIHD-TASSVARGIQFORGLQFCTRA 1420
QY 51 -----DKNDHDKHDKRKRKKKGEKQIPGEEKRKRVRVEDKKRRD 95
DB 1421 SKTLKAEGLTEIEEVEVKOKSSRRKRKSDSGSTPTTS---TSRDKDSSKKQK 1477
QY 96 RVENAEKDLQCHAPVRLDLPPEKP-----LTSSLAQEVEQTPLOFALNQLRQL 147
DB 1478 RGRPPAK-----LSPNPNTLKWKIKVDAVIKYKSSGQLSEVFQLP--- 1523
QY 148 QKDPSPAFSPPTVDFIAPGYSMTIKHPMDSTMEKIKANDYQSIIEELKDNFGLMCTNA 207
DB 1524 SRKE-----LPEYELIRKPVDPFKIKERIRNHKYSRLNDLEKDVMLLCOMA 1570
QY 208 MIVKPEPIYKAKKLLHSGMKILISOERISLQSIDFMADLQTRKQKDGTDTSOSGE 267
DB 1571 QTFNLEBSLIYEDS-----IVLOSFTSVROKIE-----KEDD-----SEGE 1607
QY 268 DGGCQOREDESDGAHAHAFKSPSKENKK--DKDMLDKPK-----S 308
DB 1608 ES-----EEEEGESESESSRSVVKYIKLGRKEKAQDRLKGRRRPSRGRAPVVD 1662
QY 309 NNLEREOQLDR 320
DB 1663 DDSEEOQE-DR 1673

RESULT 15
US-09-535-008-2
; Sequence 2, Application US/09535008
; Patent No. 6465629
; GENERAL INFORMATION:
; APPLICANT: Wong, Alexander K.C.
; APPLICANT: Tavigian, Sean V.
; APPLICANT: Teng, David H.-F.
; TITLE OF INVENTION: BGI IS A TUMOR SUPPRESSOR THAT IS MUTATED IN PROSTATE
; TITLE OF INVENTION: AND OTHER CANCER TYPES
; FILE REFERENCE: 2318-259
; CURRENT APPLICATION NUMBER: US/09/535,008
; CURRENT FILING DATE: 2000-03-23
; EARLIER APPLICATION NUMBER: U.S. 60/125,806
; EARLIER FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 2
```

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; LENGTH: 1647
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-535-008-2

Query Match
Best Local Similarity 23.1%; Score 187; DB 4; Length 1647;
Matches 77; Conservative 53; Mismatches 118; Indels 86; Gaps 14;

QY 7 KHSDDHLYEYVEKPLKLVKYGNEVTELSGSSGHDSLPEDKNDHDKHDKRKKR 66
DB 1372 RHRKEVDYDSLTKEQWLKAEGLTEIE-----BEVROKSSRRKKRD 1416
QY 67 KKEKQIPGEEKRKRVRVEDKKRRDRVENEAEKDLQCHAPVRLDLPPEKP-LTSSL 125
DB 1417 SDAGSSTPTTS---TSRDKDSSKKQKGRGPAEK-----LSPNPNTLK-- 1460
QY 126 AKQEEVEQTPLOFALNQLRQKDPSPAFSPPTVDFIAPGYSMTIKHPMDSTMEKI 185
DB 1461 -KMKKIVDAVIKYKSSSGRLS-----EVFIQLPSRREL-PEYVELIRKVPDPFKIKERI 1514
QY 186 KANDYQSIIEELKDNFGLMCTNAMIVKPEPIYKAKKLLHSGMKILISOERISLQSID 245
DB 1515 RNHKYSRLNDLEKDVMLLCQAQTFNLEBSLIYEDS-----IVLOSFTSVROKIE 1565
QY 246 FMADLQTRKQKDGTDTSQSGEDGCGQOREDESDGAHAHAFKSPSKENKK--DKDML 303
DB 1566 -----KEDD-----SEGEES-----EEEEGESESESSRSVVKYIKLGRKEKAQ 1606
QY 304 DKFK-----NNLEREOQLDR 320
DB 1607 DRLKGRRRPSRGRAPVVDSEEOQE-DR 1639

Search completed: November 27, 2003, 01:08:59
Job time : 26 secs
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